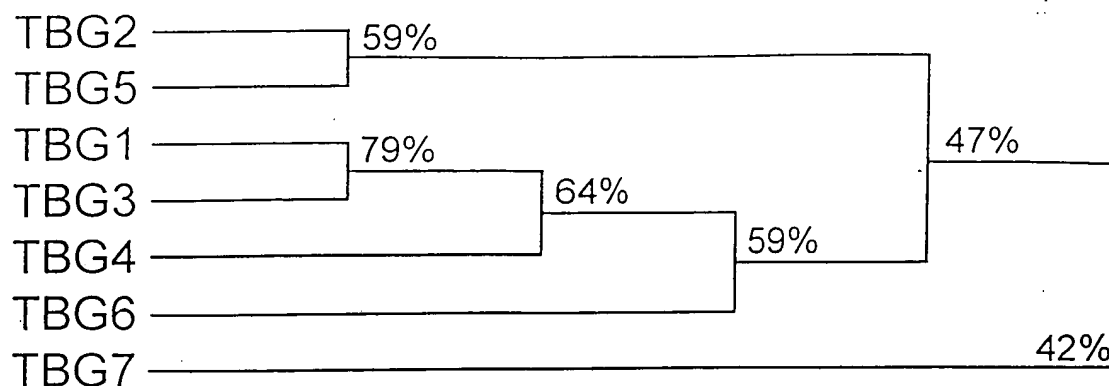




A



B

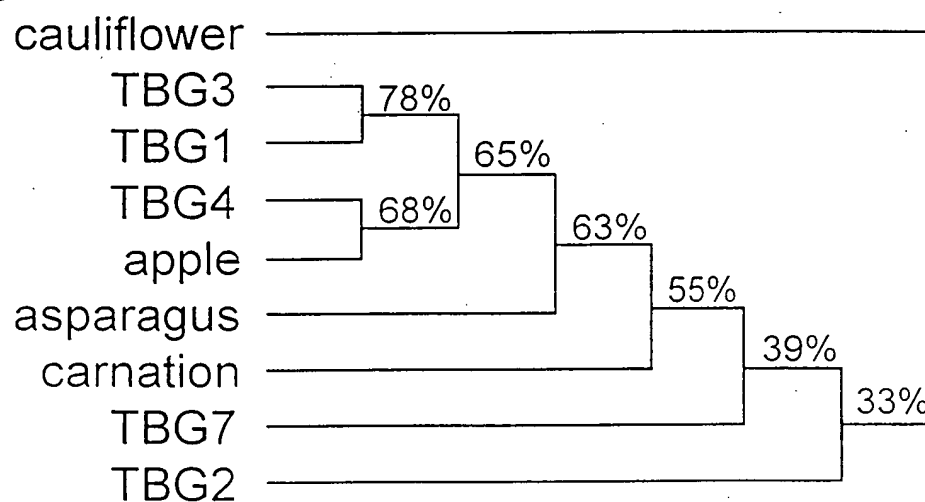
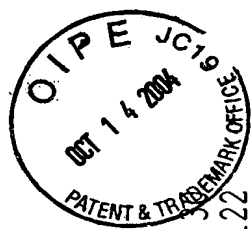


Figure 1. β -Galactosidase phylogenetic tree based on shared amino acid sequence identity. A. Tomato β -galactosidase (TBG) cDNAs. B. Plant β -galactosidases. Higgins-Sharp algorithm (UPGMA method)

FIG. I



TTTTTTCCTTGTCTCTTTTGTCTCAGCACTAG
31 AGCTAGAAGAGAAAAAGAGTATGGACTAATGAATAAACATAAAAAAGAGAGAAAAAAGAGAAAAATCTTCAGACAACA 122
123 AAAACAGCTGTTTCCCTTCACCTACTTTTTTTTCCCAATCTCTATATATTGCAAGATAGATAAAGTTTGCAACTTGATTAAAAA 214
215 GAATAATAAGCTGTGGGGTAGGGAGGAAGTTAGTTCAATTGCCTTGTAAGGCACAATCTTGATTCTTGATTGTTGACAAAT 305

306 ATG GGT TTT TGG ATG GCA ATG TTG CTG ATG TTG TTA TTG TGT TCT TGT GGA ATT GCT TCT 374
1 Met Gly Phe Trp Met Ala Met Leu Leu Met Leu Leu Cys Leu Trp Val Ser Cys Gly Ile Ala Ser 23

375 GTT TCA TAT GAC CAT AAA GCT ATC ATT GTA AAT GGA CAA AGA AAA ATT CTC ATT TCT GGA TCC ATT CAC 443
24 Val Ser Tyr Asp His Lys Ala Ile Ile Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His 46

444 TAC CCT AGA AGC ACC CCT GAG ATG TGG CCA GAT CTT ATT CAG AAG GCA AAA GAA GGG GGA GTT GAT GTT 512
47 Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu Gly Val Asp Val 69

513 ATA CAG ACT TAT GTT TTC TGG AAT GGG CAT GAG CCT GAA GAA GGG AAA TAT TAT TTT GAA GAG AGG TAT 581
70 Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Glu Glu Lys Tyr Tyr Phe Glu Glu Arg Tyr 92

582 GAT TTA GTG AAG TTC ATT AAA GTG GTG CAA GAA GCA GGA CTT TAT GTG CAT CTT AGG ATT GGA CCT TAT 650
93 Asp Leu Val Lys Phe Ile Lys Val Val Gln Glu Ala Gly Leu Tyr Val His Leu Arg Ile Gly Pro Tyr 115

651 GCA TGT GCT GAA TGG AAT TTT GGG GGT TTT CCT GTT TGG CTG AAG TAT GTT CCA GGT ATT AGT TTC AGA 719
116 Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg 138

720 ACA AAC AAT GAG CCA TTC AAG GCT GCA ATG CAA AAG TTC ACT ACT AAG ATT GTT GAT ATG ATG AAA GCA 788
139 Thr Asn Asn Glu Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys Ala 161

789 GAA AAG CTC TAT GAA ACT CAG GGT GGT CCA ATT ATT CTA TCT CAG ATA GAA AAT GAA TAT GGA CCT ATG 857
162 Glu Lys Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met 184

FIG. 2A-1

858	GAG	TGG	GAA	CTA	GGT	GAA	CCT	GGT	AAA	GTT	TAC	TCA	GAA	TGG	GCA	GCC	AAA	ATG	GCT	GTG	GAT	CTT	GGC	926
185	Glu	Trp	Glu	Leu	Gly	Glu	Pro	Gly	Lys	Val	Tyr	Ser	Glu	Trp	Ala	Ala	Lys	Met	Ala	Val	Asp	Leu	Gly	207
927	ACT	GGT	GTC	CCA	TGG	ATC	ATG	TGC	AAG	CAA	GAT	GAT	GTC	CCT	GAT	CCT	ATT	ATT	AAT	ACT	TGC	AAT	GGT	995
208	Thr	Gly	Val	Pro	Trp	Ile	Met	Cys	Lys	Gln	Asp	Val	Pro	Asp	Pro	Ile	Ile	Asn	Thr	Cys	Asn	Gly	230	
996	TTC	TAC	TGT	GAC	TAC	TTC	ACA	CCA	AAT	AAG	GCT	AAT	AAA	CCC	AAG	ATG	TGG	ACT	GAA	GCC	TGG	ACA	GCC	1064
231	Phe	Tyr	Cys	Asp	Tyr	Phe	Thr	Pro	Asn	Lys	Ala	Asn	Lys	Pro	Lys	Met	Trp	Thr	Glu	Ala	Trp	Thr	Ala	253
1065	TGG	TTT	ACC	GAA	TTT	GGA	GGT	CCA	GTT	CCT	TAC	CGT	CCT	GCA	GAG	GAT	ATG	GCA	TTT	GCT	GTC	GCA	AGA	1133
254	Trp	Phe	Thr	Glu	Phe	Gly	Gly	Pro	Val	Pro	Tyr	Arg	Pro	Ala	Glu	Asp	Met	Ala	Phe	Ala	Val	Ala	Arg	276
1134	TTT	ATA	CAA	ACG	GGA	GGC	TCC	TTC	ATC	AAT	TAC	TAT	ATG	TAT	CAT	GGA	GGA	ACA	AAC	TTT	GGA	AGG	ACT	1202
277	Phe	Ile	Gln	Thr	Gly	Gly	Ser	Phe	Ile	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	299
1203	TCT	GGT	GGC	CCA	TTT	ATT	GCT	ACT	AGT	TAT	GAT	TAT	GAT	GCA	CCC	CTA	GAT	GAA	TTT	GGG	TCA	TTA	CGG	1271
300	Ser	Gly	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Phe	Gly	Ser	Leu	Arg	322
1272	CAG	CCT	AAA	TGG	GGT	CAT	CTG	AAA	GAT	CTA	CAT	AGA	GCA	ATA	AAG	CTC	TGT	GAG	CCA	GCT	TTA	GTA	TCT	1340
323	Gln	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	His	Arg	Ala	Ile	Lys	Leu	Cys	Glu	Pro	Ala	Leu	Val	Ser	345
1341	GTA	GAT	CCA	ACT	GTG	ACA	TCC	TTA	GGA	AAC	TAT	CAA	GAG	GCA	CGT	GTT	TTC	AAG	TCA	GAG	TCT	GGG	GCC	1409
346	Val	Asp	Pro	Thr	Val	Thr	Ser	Ser	Leu	Gly	Asn	Tyr	Gln	Ala	Arg	Val	Phe	Lys	Ser	Glu	Ser	Gly	Ala	368
1410	TGC	GCT	GCC	TTC	CTA	GCA	AAT	TAC	AAC	CAG	CAC	TCT	TTT	GCT	AAA	GTG	GCA	TTT	GGG	AAC	ATG	CAT	TAT	1478
369	Cys	Ala	Ala	Phe	Leu	Ala	Asn	Tyr	Asn	Gln	His	Ser	Phe	Ala	Lys	Val	Ala	Phe	Gly	Asn	Met	His	Tyr	391

FIG. 2A-2

1479	AAC	TTG	CCA	CCC	TGG	TCT	ATC	AGC	ATT	CTT	CCC	GAC	TGC	AAG	AAC	ACT	GTC	TAT	AAT	ACT	GCA	AGG	GTT	1547	
392	Asn	Leu	Pro	Pro	Trp	Ser	Ile	Ser	Ile	Leu	Pro	Asp	Cys	Lys	Asn	Thr	Val	Try	Asn	Thr	Ala	Arg	Val	414	
1548	GGT	GCT	CAA	AGT	GCT	CAG	ATG	AAG	ATG	ACT	CCA	GTC	AGT	AGA	GGA	TTC	TCA	TGG	GAG	TCA	TTC	AAT	GAA	1616	
415	Gly	Ala	Gln	Ser	Ala	Gln	Met	Lys	Met	Thr	Pro	Pro	Val	Ser	Arg	Gly	Phe	Ser	Trp	Glu	Ser	Phe	Asn	Glu	437
1617	GAC	GCA	GCA	TCG	CAT	GAA	GAC	GAC	ACT	TTC	ACA	GTT	GTT	GGG	TTA	TTG	GAG	CAG	ATT	AAT	ATC	ACA	AGA	1685	
438	Asp	Ala	Ala	Ser	His	Glu	Asp	Asp	Thr	Phe	Thr	Val	Val	Gly	Leu	Leu	Glu	Gln	Ile	Asn	Ile	Thr	Arg	460	
1686	GAT	GTA	TCT	GAT	TAC	TTG	TGG	TAT	ATG	ACT	GAC	ATT	GAG	ATT	GAT	CCA	ACA	GAA	GGA	TTT	TTG	AAT	AGT	1754	
461	Asp	Val	Ser	Asp	Tyr	Leu	Trp	Tyr	Met	Thr	Asp	Ile	Glu	Ile	Asp	Pro	Thr	Glu	Gly	Phe	Leu	Asn	Ser	483	
1755	GGA	AAT	TGG	CCT	TGG	CTT	ACT	GTC	TTT	TCT	GCT	GGC	CAT	GCA	TTG	CAT	GTA	TTC	GTG	AAT	GGT	CAA	TTA	1823	
484	Gly	Asn	Trp	Pro	Trp	Leu	Thr	Val	Phe	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn	Gly	Gln	Leu	506	
1824	GCA	GGA	ACT	GTG	TAC	GGA	AGT	TTA	GAA	AAC	CCA	AAA	CTA	ACT	TTC	AGC	AAC	GGT	ATA	AAT	CTG	AGA	GCT	1892	
507	Ala	Gly	Thr	Val	Tyr	Gly	Ser	Leu	Glu	Asn	Pro	Lys	Leu	Thr	Phe	Ser	Asn	Gly	Ile	Asn	Leu	Arg	Ala	529	
1893	GGT	GTG	AAC	AAG	ATT	TCT	CTG	CTA	AGC	ATT	GCT	GTT	GGT	CTT	CCG	AAC	GTT	GGC	CCT	CAT	TTT	GAG	ACA	1961	
530	Gly	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Val	Gly	Pro	His	Phe	Glu	Thr	552	
1962	TGG	AAT	GCT	GGT	GTT	CTT	GGA	CCA	GTT	TCA	CTT	AAT	GGA	ACA	AGA	GAT	TTA	ACA	TGG					2030	
553	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Val	Ser	Leu	Asn	Gly	Leu	Asn	Glu	Gly	Thr	Arg	Asp	Leu	Thr	Trp	575	
2031	CAG	AAA	TGG	TTC	TAC	AAG	GTT	GGT	CTA	AAA	GGA	GCC	CTG	AGT	CTT	CAT	TCA	CTC	AGT	GGT	AGC	CCA		2099	
576	Gln	Lys	Trp	Phe	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	Ser	Gly	Ser	Pro	598	

FIG. 2A-3

2100	TCC	GTG	GAG	TGG	GTG	GAA	GGC	TCT	TTA	GTG	GCT	CAG	AAG	CAG	CCA	CTC	AGT	TGG	TAT	AAG	ACT	ACA	TTC	2168
599	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Lys	Gln	Pro	Leu	Ser	Trp	Tyr	Lys	Thr	Thr	Phe	621
2169	AAT	GCT	CCA	GAT	GGA	AAT	GAA	CCT	TTG	GCT	TTA	GAT	ATG	AAT	ACC	ATG	GGC	AAA	GGT	CAA	GTA	TGG	ATA	2237
622	Asn	Ala	Pro	Asp	Gly	Asn	Glu	Pro	Leu	Ala	Leu	Asp	Met	Asn	Thr	Met	Gly	Lys	Gly	Gln	Val	Trp	Ile	644
2238	AAT	GGT	CAG	AGC	CTC	GGA	CGC	CAC	TGG	CCT	GCA	TAT	AAA	TCA	TCT	GGA	AGT	TGT	AGT	GTC	TGT	AAC	TAT	2306
645	Asn	Gly	Gln	Ser	Leu	Gly	Arg	His	Trp	Pro	Ala	Tyr	Lys	Ser	Ser	Gly	Ser	Cys	Ser	Val	Cys	Asn	Tyr	667
2307	ACT	GGC	TGG	TTT	GAT	GAG	AAA	AAG	TGC	CTA	ACT	AAC	TGT	GGT	GAG	GGC	TCA	CAA	AGA	TGG	TAC	CAC	GTA	2375
668	Thr	Gly	Trp	Phe	Asp	Glu	Lys	Lys	Cys	Leu	Thr	Asn	Cys	Gly	Glu	Gly	Ser	Gln	Arg	Trp	Tyr	His	Val	690
2376	CCC	CGG	TCT	TGG	CTG	TAT	CCT	ACT	GGA	AAT	TTG	TTA	GTT	GTA	TTC	GAG	GAA	TGG	GGA	GGA	GAT	CCT	TAT	2444
691	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Val	Phe	Glu	Glu	Trp	Gly	Gly	Asp	Pro	Tyr	713
2445	GGA	ATC	ACT	TTA	GTC	AAA	AGA	GAA	ATA	GGG	AGT	GTT	TGT	GCT	GAT	ATA	TAT	GAG	TGG	CAA	CCA	CAG	TTA	2513
714	Gly	Ile	Thr	Leu	Val	Lys	Arg	Glu	Ile	Gly	Ser	Val	Cys	Ala	Asp	Ile	Tyr	Glu	Trp	Gln	Pro	Gln	Leu	736
2514	TTG	AAT	TGG	CAG	AGG	CTA	GTA	TCT	GGT	AAG	TTT	GAC	AGA	CCT	CTC	AGA	CCT	AAA	GCC	CAT	CTT	AAG	TGT	2582
737	Leu	Asn	Trp	Gln	Arg	Leu	Val	Ser	Gly	Lys	Phe	Asp	Arg	Pro	Leu	Arg	Pro	Lys	Ala	His	Leu	Lys	Cys	759
2583	GCA	CCT	GGT	CAG	AAG	ATT	TCT	TCA	ATC	AAA	TTT	GCA	AGC	TTT	GGA	ACA	CCA	GAG	GGA	GTT	TGT	GGG	AAC	2651
760	Ala	Pro	Gly	Gln	Lys	Ile	Ser	Ser	Ile	Lys	Phe	Ala	Ser	Phe	Gly	Thr	Pro	Glu	Gly	Val	Cys	Gly	Asn	782
2652	TTC	CAG	CAG	GGA	AGC	TGC	CAT	GCT	CCG	CGC	TCA	TAT	GAT	GCT	TTC	AAA	AAG	AAT	TGT	GTT	GGG	AAA	GAG	2720
783	Phe	Gln	Gln	Gly	Ser	Cys	His	Ala	Pro	Arg	Ser	Tyr	Asp	Ala	Phe	Lys	Lys	Asn	Cys	Val	Gly	Lys	Glu	805

FIG. 2A-4

2721	TCT TGC TCA GTA CAG GTA ACA CCA GAG AAT TTT GGA GGT GAT CCA TGT CGA AAC GTT CTA AAG AAA CTC	2789
806	Ser Cys Ser Val Gln Val Thr Pro Glu Asn Phe Gly Gly Asp Pro Cys Arg Asn Val Leu Lys Lys Leu	828
2790	TCA GTG GAA GCC ATT TGT AGT TGA TGATTCTGAGTATACAAGTGAAAAAATACTTGAACCACTCATATAAACATTTTTCAAACG	2873
829	Ser Val Glu Ala Ile Cys Ser ***	836
2874	AGCTACTAGACATCCATTAAACCCACACTACCATTTTTTGGCTTTTGCTGGGGTTGAAGTTGTACAGTTAAGCAACACACCTCTTTGATCAAAG	2965
2966	CTCACCTGATTATGAAGATGATTGACGAAAGATTCTGTACATGTAAAGTTTCGTCTAATTACACATACAGATATGATTCTTGATGAATCGAT	3057
3058	GTGCAAAATTTTGTGTTAGGGTGAGAGAGACTTGAAAAGCATTTGGCTTTCATGATGTTCTACATTATACAATCATAATGTAAGTAAGC	3149
3150	AAGCAATAATTCATTGCTTTGCACATTGAAAATGCAATTTTACTATGTTGCAGTACAAAAAATAAAAAA	3224

FIG. 2A-5

348	CTC	TTT	ATT	CGA	ATA	GGT	CCT	TAT	GCC	TGT	GCA	GAA	TGG	AAC	TTC	GGG	GGA	TTC	CCC	ATA	TGG	CTT	CGT	416
116	Leu	Phe	Ile	Arg	Ile	Gly	Pro	Tyr	Ala	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Ile	Trp	Leu	Arg	138
417	GAT	ATA	CCT	GGA	ATA	GAA	TTT	CGA	ACA	GAT	AAT	GCA	CCA	TTC	AAG	GAG	GAG	ATG	GAG	CGC	TAT	GTT	AAA	485
139	Asp	Ile	Pro	Gly	Ile	Glu	Phe	Arg	Thr	Asp	Asn	Ala	Pro	Phe	Lys	Glu	Glu	Met	Glu	Arg	Tyr	Val	Lys	161
486	AAG	ATA	GTT	GAT	CTT	ATG	ATA	TCT	GAG	TCG	CTC	TTT	TCG	TGG	CAA	GGT	GGT	CCT	ATC	ATT	TTG	CTG	CAG	554
162	Lys	Ile	Val	Asp	Leu	Met	Ile	Ser	Glu	Ser	Glu	Phe	Ser	Trp	Gln	Gly	Gly	Pro	Ile	Ile	Leu	Leu	Gln	184
555	ATT	GAA	AAT	GAA	TAT	GGA	AAT	GTT	GAA	AGC	TCA	TTC	GGT	CCC	AAG	GGG	AAG	TTA	TAT	ATG	AAA	TGG	GCT	623
185	Ile	Glu	Asn	Glu	Tyr	Gly	Asn	Val	Glu	Ser	Ser	Phe	Gly	Pro	Lys	Gly	Lys	Leu	Tyr	Met	Lys	Trp	Ala	207
624	GCT	GAA	ATG	GCT	GTT	GGT	CTT	GGT	GCT	GGT	GTT	CCA	TGG	GTC	ATG	TGC	AGG	CAA	ACT	GAT	GCT	CCA	GAA	692
208	Ala	Glu	Met	Ala	Val	Gly	Leu	Gly	Ala	Gly	Val	Pro	Trp	Val	Met	Cys	Arg	Gln	Thr	Asp	Ala	Pro	Glu	230
693	TAC	ATC	ATA	GAT	ACT	TGT	AAT	GCA	TAC	TAT	TGT	GAT	GGG	TTC	ACG	CCG	AAT	TCC	GAG	AAG	AAA	CCG	AAA	761
231	Tyr	Ile	Ile	Asp	Thr	Cys	Asn	Ala	Tyr	Tyr	Cys	Asp	Gly	Phe	Thr	Pro	Asn	Ser	Glu	Lys	Lys	Pro	Lys	253
762	ATT	TGG	ACT	GAG	AAT	TGG	AAT	GGA	TGG	TTT	GCA	GAT	TGG	GGT	GAA	AGA	CTT	CCA	TAT	AGA	CCT	TCC	GAG	830
254	Ile	Trp	Thr	Glu	Asn	Trp	Asn	Gly	Trp	Phe	Ala	Asp	Trp	Gly	Glu	Arg	Leu	Pro	Tyr	Arg	Pro	Ser	Glu	276
831	GAT	ATT	GCA	TTT	GCA	ATT	GCT	CGT	TTC	TTT	CAA	CGT	GGG	GGC	AGC	TTA	CAG	AAC	TAT	TAT	ATG	TAT	TTT	899
277	Asp	Ile	Ala	Phe	Ala	Ile	Ala	Arg	Phe	Phe	Gln	Arg	Gly	Gly	Ser	Leu	Gln	Asn	Tyr	Tyr	Met	Tyr	Phe	299
900	GGT	GGG	ACA	AAT	TTT	GGC	CGG	ACT	GCT	GGT	GGC	CCA	ACT	CAA	ATC	ACT	AGC	TAT	GAT	TAT	GAT	GCT	CCA	968
300	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	Ala	Gly	Gly	Pro	Thr	Gln	Ile	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	322

FIG. 2B-2

969	CTG	GAT	GAA	TAT	GGA	CTA	CTA	CGT	CAA	CCT	AAA	TGG	GGC	CAT	TTG	AAG	GAT	CTG	CAT	GCT	GCT	ATA	AAG	1037
323	Leu	Asp	Glu	Tyr	Gly	Leu	Leu	Arg	Gln	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	His	Ala	Ala	Ile	Lys	345
1038	CTT	TGT	GAA	CCA	GCT	CTT	GTT	GCT	GCT	GAT	TCA	CCT	CAG	TAT	ATT	AAA	CTG	GGA	CCA	AAA	CAG	GAG	GCA	1106
346	Leu	Cys	Glu	Pro	Ala	Leu	Val	Ala	Ala	Asp	Ser	Pro	Gln	Tyr	Ile	Lys	Leu	Gly	Pro	Lys	Gln	Glu	Ala	345
1107	CAT	GTC	TAT	CGT	GGA	ACA	TCC	AAC	AAC	ATT	GGC	CAA	TAT	ATG	TCC	TTA	AAT	GAA	GGC	ATA	TGC	GCA	GCA	1175
369	His	Val	Tyr	Arg	Gly	Thr	Ser	Asn	Asn	Ile	Gly	Gln	Tyr	Met	Ser	Leu	Asn	Glu	Gly	Ile	Cys	Ala	Ala	391
1176	TTT	ATT	GCA	AAT	ATT	GAT	GAA	CAT	GAA	TCA	GCA	ACA	GTG	AAA	TTT	TAC	GGT	CAA	GAG	TTC	ACT	TTA	CCT	1244
392	Phe	Ile	Ala	Asn	Ile	Asp	Glu	His	Glu	Ser	Ala	Thr	Val	Lys	Phe	Tyr	Gly	Gln	Glu	Phe	Thr	Leu	Pro	414
1245	CCA	TGG	TCA	GTG	GTA	TTC	TGC	CAG	ATT	GCA	GAA	ATA	CAG	CTT	TCA	ACA	CAG	CTA	AGG	TGG	GGG	CAC	AAA	1313
415	Pro	Trp	Ser	Val	Val	Phe	Cys	Gln	Ile	Ala	Glu	Ile	Gln	Leu	Ser	Thr	Gln	Leu	Arg	Trp	Gly	His	Lys	437
1314	CTT	CAA	TCA	AAA	CAG	TGG	GCT	CAG	ATT	CTG	TTT	CAG	TTG	GGA	ATA	ATT	CTT	TGT	TTC	TAC	AAG	TTA	TCA	1382
438	Leu	Gln	Ser	Lys	Gln	Trp	Ala	Gln	Ile	Leu	Phe	Gln	Leu	Gly	Ile	Ile	Leu	Cys	Phe	Tyr	Lys	Leu	Ser	460
1383	CTA	AAA	GCA	AGC	TCG	GAA	AGT	TTT	TCA	CAA	TCT	TGG	ATG	ACA	TTG	AAG	GAG	CCA	CTT	GGT	GTG	TGG	GGT	1451
461	Leu	Lys	Ala	Ser	Ser	Glu	Ser	Phe	Ser	Gln	Ser	Trp	Met	Thr	Leu	Lys	Glu	Pro	Leu	Gly	Val	Trp	Gly	483
1452	GAC	AAG	AAT	TTC	ACT	TCT	AAA	GGA	ATA	CTG	GAG	CAT	CTG	AAT	GTG	ACA	AAA	GAC	CAG	TCT	GAT	TAC	CTG	1520
484	Asp	Lys	Asn	Phe	Thr	Ser	Lys	Gly	Ile	Leu	Glu	His	Leu	Asn	Val	Thr	Lys	Asp	Gln	Ser	Asp	Tyr	Leu	506
1521	TGG	TAT	CTG	ACC	AGG	ATA	TAT	ATT	TCT	GAT	GAT	GAC	ATC	TCA	TTT	TGG	GAG	GAA	AAT	GAT	GTT	AGT	CCA	1589
507	Trp	Tyr	Leu	Thr	Arg	Ile	Tyr	Ile	Ser	Asp	Asp	Asp	Ile	Ser	Phe	Trp	Glu	Glu	Asn	Asp	Val	Ser	Pro	529

FIG. 2B-3

1590	ACA	ATT	GAT	ATT	GAT	AGC	ATG	CGT	GAT	TTT	GTT	CGC	ATT	TTT	GTT	AAT	GGG	CAG	CTT	GCA	GGT	AGT	GTG	1658
530	Thr	Ile	Asp	Ile	Asp	Ser	Met	Arg	Asp	Phe	Val	Arg	Ile	Phe	Val	Asn	Gly	Gln	Leu	Ala	Gly	Ser	Val	552
1659	AAA	GGC	AAA	TGG	ATC	AAG	GTG	GTT	CAA	CCT	GTT	AAG	CTG	GTT	CAG	GGG	TAC	AAC	GAC	ATA	CTG	CTA	TTA	1727
553	Lys	Gly	Lys	Trp	Ile	Lys	Val	Val	Gln	Pro	Val	Lys	Leu	Val	Gln	Gly	Tyr	Asn	Asp	Ile	Leu	Leu	Leu	575
1728	TCT	GAG	ACG	GTG	GGA	TTG	CAG	AAT	TAT	GGT	GCC	TTC	TTG	GAG	AAG	GAT	GGG	GCA	GGT	TTT	AAA	GGT	CAG	1796
576	Ser	Glu	Thr	Val	Gly	Leu	Gln	Asn	Tyr	Gly	Ala	Phe	Leu	Glu	Lys	Asp	Gly	Ala	Gly	Phe	Lys	Gly	Gln	598
1797	ATA	AAG	CTT	ACA	GGA	TGC	AAA	AGC	GGG	GAT	ATC	AAT	CTC	ACA	ACA	TCT	TTA	TGG	ACC	TAC	CAG	GTG	GGG	1865
599	Ile	Lys	Leu	Thr	Gly	Cys	Lys	Ser	Gly	Asp	Ile	Asn	Leu	Thr	Thr	Ser	Leu	Trp	Thr	Tyr	Gln	Val	Gly	621
1866	CTT	AGA	GGC	GAA	TTC	CTG	GAA	GTA	TAT	GAT	GTC	AAAT	AGT	ACT	GAA	AGT	GCA	GGA	TGG	ACT	GAG	TTT	CCC	1934
622	Leu	Arg	Gly	Glu	Phe	Leu	Glu	Val	Tyr	Asp	Val	Asn	Ser	Thr	Glu	Ser	Ala	Gly	Trp	Thr	Glu	Phe	Pro	644
1935	ACT	GGT	ACA	ACT	CCG	TCA	GTC	TTT	TCG	TGG	TAC	AAG	ACA	AAG	TTT	GAT	GCC	CCA	GGC	GGG	ACA	GAT	CCA	2003
645	Thr	Gly	Thr	Thr	Pro	Ser	Val	Phe	Ser	Trp	Tyr	Lys	Thr	Lys	Phe	Asp	Ala	Pro	Gly	Gly	Thr	Asp	Pro	667
2004	GTT	GCT	CTT	GAT	TTT	AGT	AGC	ATG	GGA	AAA	GGT	CAG	GCA	TGG	GTT	AAT	GGC	CAC	CAT	GTA	GGA	AGA	TAT	2072
668	Val	Ala	Leu	Asp	Phe	Ser	Ser	Met	Gly	Lys	Gly	Gln	Ala	Trp	Val	Asn	Gly	His	His	Val	Gly	Arg	Tyr	690
2073	TGG	ACT	TTG	GTT	GCA	CCA	AAT	AAT	GGA	TGT	GGA	AGA	ACT	TGT	GAT	TAT	CGT	GGT	GCT	TAC	CAC	TCT	GAT	2141
691	Trp	Thr	Leu	Val	Ala	Pro	Asn	Asn	Gly	Cys	Gly	Arg	Thr	Cys	Asp	Tyr	Arg	Gly	Ala	Tyr	His	Ser	Asp	713
2142	AAA	TGT	AGG	ACA	AAC	TGT	GGA	GAG	ATT	ACT	CAG	GCC	TGG	TAC	CAT	ATA	CCT	AGA	TCA	TGG	CTA	AAG	ACA	2210
714	Lys	Cys	Arg	Thr	Asn	Cys	Gly	Glu	Ile	Thr	Gln	Ala	Trp	Tyr	His	Ile	Pro	Arg	Ser	Trp	Leu	Lys	Thr	736

FIG. 2B-4

2211	TTA AAT AAT GTA CTA GTT ATC TTT GAA GAA ACA GAT AAA ACT CCG TTT GAT ATT TCC ATT TCT ACG CGT	2279
737	Leu Asn Asn Val Leu Val Ile Phe Glu Glu Thr Asp Lys Thr Pro Phe Asp Ile Ser Ile Ser Thr Arg	759
2280	TCT ACT GAA ACC ATT TGT GCT CAA GTA TCG GAA AAG CAC TAT CCA CCT CTA CAT AAG TGG TCT CAT TCG	2348
760	Ser Thr Glu Thr Ile Cys Ala Gln Val Ser Glu Lys His Tyr Pro Pro Leu His Lys Trp Ser His Ser	782
2349	GAG TTT GAC AGA AAG TTG TCT CTG ATG GAT AAA ACA CCA GAA ATG CAC TTG CAG TGT GAC GAA GGA CAT	2417
783	Glu Phe Asp Arg Lys Leu Ser Leu Met Asp Lys Thr Pro Glu Met His Leu Gln Cys Asp Glu Gly His	805
2418	ACA ATC TCT TCT ATT GAA TTT GCA AGC TAT GGA AGT CCG AAT GGC AGC TGT CAA AAG TTC TCA CAA GGA	2486
806	Thr Ile Ser Ser Ile Glu Phe Ala Ser Tyr Gly Ser Pro Asn Gly Ser Cys Gln Lys Phe Ser Gln Gly	828
2487	AAA TGC CAT GCT GCA AAT TCC TTG TCT GTT GTA TCT CAG GCT TGT ATA GGA AGA ACT AGT TGC AGC ATT	2555
829	Lys Cys His Ala Ala Asn Ser Leu Ser Val Val Ser Gln Ala Cys Ile Gly Arg Thr Ser Cys Ser Ile	851
2556	GGC ATT TCC AAT GGT GTA TTT GGA GAT CCA TGT CGA CAC GTT GTG AAG AGT TTG GCT GTT CAA GCA AAA	2624
852	Gly Ile Ser Asn Gly Val Phe Gly Asp Pro Cys Arg His Val Lys Ser Leu Ala Val Gln Ala Lys	874
2625	TGC TCA CCA CCA GAC CTC AGC ACT TCA GCT TCC TCG TGA GGAGACTCTGGTAACACGTTAACCTTTTAGAACGAA	2702
875	Cys Ser Pro Pro Pro Asp Leu Ser Thr Ser Ala Ser Ser ***	888
2703	ACGATCCCTTAAAGTCCACTCGTTCCCCCTGCCCCGAGCCCTCTGCTACATTTCTCAGATCGCATCGTTACAATCAGCGGAGAAAAACGTAC	2794
2795	ATGGACGATTTTACTTGTAATAATTTGGTTACTGTATATAAATGAAAGGAATAATGTTGCTTATGCATATGAGCTGCAAATTATATGACAA	2886
2887	AGTAACAAATGAAAATAGAAAACCTCCTGTCTGTCAAAGAATTTTAAACAACACCATTTATTAAAAGTTAGTTAACATGATTAAAAA	2978
2979	AAAAAA	2984

FIG. 2B-5

1	AGAGTTCATTATTTT	30
31	AAGAGGAAAAAATAAGTTAAAGGGGGGAAAAAGTTTTCATTTTGGCCTTAAAAAGGCACAAATCTTGATAGAAAAAGGAGATAATTTTAC	121
122	ATG GGT TGT ACG CTT ATA CTA ATG TTG AAT GTG TTG TTT GGT TCA TGG GTT TTT TCT GGA	190
1	Met Gly Cys Thr Leu Ile Leu Met Leu Asn Val Leu Leu Val Leu Gly Ser Trp Val Phe Ser Gly	23
191	ACA GCT TCT GTT TCA TAT GAC CAT AGG GCT ATT ATT GTA AAT GGA CAA AGA AGA ATA CTT ATT TCT GGT	259
24	Thr Ala Ser Val Ser Tyr Asp His Arg Ala Ile Ile Val Asn Gly Gln Arg Arg Ile Leu Ile Ser Gly	46
260	TCT GTT CAT TAT CCA AGA AGC ACT CCT GAG ATG TGG CCA GGT ATT ATT CAA AAG GCT AAA GAA GGA GGT	328
47	Ser Val His Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Gly Ile Ile Gln Lys Ala Lys Glu Gly Gly	69
329	GTG GAT GTG ATT CAG ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT CAA CAA GGG AAA TAT TAT TTT GAA	397
70	Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Gln Gln Gly Lys Tyr Tyr Phe Glu	92
398	GGG AGA TAT GAT TTA GTG AAG TTT ATT AAG CTG GTG CAC CAA GCA GGA CTT TAT GTC CAT CTT AGA GTT	466
93	Gly Arg Tyr Asp Leu Val Lys Phe Ile Lys Leu Val His Gln Ala Gly Leu Tyr Val His Leu Arg Val	115
467	GGA CCT TAT GCT TGT GCT GAA TGG AAT TTT GGG GGC TTT CCT GTT TGG CTG AAA TAT GTT CCA GGT ATC	535
116	Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile	138
536	AGT TTC AGA ACA GAT AAT GGA CCT TTC AAG GCT GCA ATG CAA AAA TTT ACT GCC AAG ATT GTC AAT ATG	604
139	Ser Phe Arg Thr Asp Asn Gly Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Ala Lys Ile Val Asn Met	161
605	ATG AAA GCG GAA CGT TTG TAT GAA ACT CAA GGG GGC CCA ATA ATT TTA TCT CAG ATT GAG AAT GAA TAT	673
162	Met Lys Ala Glu Arg Leu Tyr Glu Thr Gln Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr	184

FIG. 2C-1

674	GGA	CCC	ATG	GAA	TGG	GAA	CTG	GGA	GCA	CCA	GGT	AAA	TCT	TAC	GCA	CAG	TGG	GCC	GCC	AAA	ATG	GCT	GTG	742
185	Gly	Pro	Met	Glu	Trp	Glu	Leu	Gly	Ala	Pro	Gly	Lys	Ser	Tyr	Ala	Gln	Trp	Ala	Ala	Lys	Met	Ala	Val	207
743	GGT	CTT	GAC	ACT	GGT	GTC	CCA	TGG	GTT	ATG	TGC	AAG	CAA	GAC	GAT	GCC	CCT	GAT	CCT	ATT	ATA	AAT	GCT	811
208	Gly	Leu	Asp	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Lys	Gln	Asp	Ala	Pro	Asp	Pro	Ile	Ile	Asn	Ala	230	
812	TGC	AAT	GGC	TTC	TAC	TGT	GAC	TAC	TTT	TCT	CCA	AAC	AAG	GCT	TAT	AAA	CCA	AAG	ATA	TGG	ACT	GAA	GCC	880
231	Cys	Asn	Gly	Phe	Tyr	Cys	Asp	Tyr	Phe	Ser	Pro	Asn	Lys	Ala	Tyr	Lys	Pro	Lys	Ile	Trp	Thr	Glu	Ala	253
881	TGG	ACT	GCA	TGG	TTT	ACT	GGT	TTT	GGA	AAT	CCA	GTT	CCT	TAC	CGT	CCT	GCT	GAG	GAC	TTG	GCA	TTT	TCT	949
254	Trp	Thr	Ala	Trp	Phe	Thr	Gly	Phe	Gly	Asn	Pro	Val	Pro	Tyr	Arg	Pro	Ala	Glu	Asp	Leu	Ala	Phe	Ser	276
950	GTT	GCA	AAA	TTT	ATA	CAG	AAG	GGA	GGT	TCC	TTC	ATC	AAT	TAT	TAC	ATG	TAT	CAT	GGA	GGA	ACA	AAC	TTT	1018
277	Val	Ala	Lys	Phe	Ile	Gln	Lys	Gly	Gly	Ser	Phe	Ile	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	299
1019	GGA	CGG	ACT	GCT	GGT	GGT	CCA	TTT	ATT	GCT	ACT	AGT	TAT	GAC	TAT	GAT	GCA	CCA	CTT	GAT	GAA	TAT	GGA	1087
300	Gly	Arg	Thr	Ala	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr	Gly	322	
1088	TTA	TTG	CGA	CAA	CCA	AAA	TGG	GGT	CAC	CTG	AAA	GAT	CTG	CAT	AGA	GCA	ATA	AAG	CTT	TGT	GAA	CCA	GCT	1156
323	Leu	Leu	Arg	Gln	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	His	Arg	Ala	Ile	Lys	Leu	Cys	Glu	Pro	Ala	345
1157	TTA	GTC	TCT	GGA	GAT	CCA	GCT	GTG	ACA	GCA	CTT	GGA	CAC	CAG	CAG	GAG	GCC	CAT	GTT	TTT	AGG	TCG	AAG	1225
346	Leu	Val	Ser	Gly	Asp	Pro	Ala	Val	Thr	Ala	Leu	Gly	His	Gln	Gln	Glu	Ala	His	Val	Phe	Arg	Ser	Lys	368
1226	GCT	GGC	TCT	TGT	GCT	GCA	TTC	CTT	GCT	AAC	TAC	GAC	CAA	CAC	TCT	TTT	GCT	ACT	GTG	TCA	TTT	GCA	AAC	1294
369	Ala	Gly	Ser	Cys	Ala	Ala	Phe	Leu	Ala	Asn	Tyr	Asp	Gln	His	Ser	Phe	Ala	Thr	Val	Ser	Phe	Ala	Asn	391

FIG. 2C-2

1295	AGG	CAT	TAC	AAC	TTG	CCA	CCA	TGG	TCA	ATC	AGC	ATT	CTT	CCC	GAC	TGC	AAG	AAC	ACT	GTA	TTT	AAT	ACA	1363
392	Arg	His	Tyr	Asn	Leu	Pro	Pro	Trp	Ser	Ile	Ser	Ile	Leu	Pro	Asp	Cys	Lys	Asn	Thr	Val	Phe	Asn	Thr	414
1364	GCA	CGG	ATC	GGT	GCT	CAA	AGT	GCT	CAG	ATG	AAG	ATG	ACT	CCA	GTC	AGC	AGA	GGA	TTG	CCC	TGG	CAG	TCA	1432
415	Ala	Arg	Ile	Gly	Ala	Gln	Ser	Ala	Gln	Met	Lys	Met	Thr	Pro	Val	Ser	Arg	Gly	Leu	Pro	Trp	Gln	Ser	437
1433	TTC	AAT	GAA	GAG	ACA	TCA	TCT	TAT	GAA	GAC	AGT	AGT	TTT	ACA	GTT	GTT	GGG	CTA	TTG	GAA	CAG	ATA	AAT	1501
438	Phe	Asn	Glu	Glu	Thr	Ser	Ser	Tyr	Glu	Asp	Ser	Ser	Phe	Thr	Val	Val	Gly	Leu	Glu	Gln	Ile	Asn		460
1502	ACA	ACA	AGA	GAC	GTG	TCT	GAT	TAT	TTG	TGG	TAT	TCA	ACA	GAT	GTC	AAG	ATT	GAT	TCA	AGA	GAA	AAG	TTT	1570
461	Thr	Thr	Arg	Asp	Val	Ser	Asp	Tyr	Leu	Trp	Tyr	Ser	Thr	Asp	Val	Lys	Ile	Asp	Ser	Arg	Glu	Lys	Phe	483
1571	TTG	AGA	GGC	GGA	AAA	TGG	CCT	TGG	CTT	ACG	ATC	ATG	TCA	GCT	GGG	CAT	GCA	TTG	CAT	GTT	TTT	GTG	AAT	1639
484	Leu	Arg	Gly	Gly	Lys	Trp	Pro	Trp	Leu	Thr	Ile	Met	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn	506
1640	GGT	CAA	TTA	GCA	GGA	ACT	GCA	TAT	GGA	AGT	TTA	GAA	AAA	CCG	AAA	CTA	ACT	TTC	AGT	AAA	GCC	GTA	AAT	1708
507	Gly	Gln	Leu	Ala	Gly	Thr	Ala	Tyr	Gly	Ser	Leu	Glu	Lys	Pro	Lys	Leu	Thr	Phe	Ser	Lys	Ala	Val	Asn	529
1709	CTG	AGA	GCA	GGT	GTT	AAC	AAG	ATT	TCT	CTA	CTG	AGC	ATT	GCT	GTT	GGC	CTT	CCG	AAT	ATC	GGC	CCA	CAT	1777
530	Leu	Arg	Ala	Gly	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Ile	Gly	Pro	His	552
1778	TTT	GAG	ACA	TGG	AAT	GCT	GGT	GTT	CTT	GGG	CCA	GTC	TCA	CTA	ACT	GGT	CTT	GAC	GAG	GGG	AAA	AGA	GAT	1846
553	Phe	Glu	Thr	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Val	Ser	Leu	Thr	Gly	Leu	Asp	Glu	Gly	Lys	Arg	Asp	575
1847	TTA	ACA	TGG	CAG	AAA	TGG	TCT	TAC	AAG	GTT	GGT	CTA	AAA	GGA	GAA	GCC	TTG	AGC	CTC	CAT	TCA	CTC	AGT	1915
576	Leu	Thr	Trp	Gln	Lys	Trp	Ser	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	Ser	598

FIG. 2C-3

1916	GGT	AGC	TCG	TCA	GTT	GAG	TGG	GTC	GAG	GGT	TCT	TTA	GTG	GCT	CAG	AGA	CAG	CCA	CTC	ACA	TGG	TAC	AAG	1984	
599	Gly	Ser	Ser	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Arg	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	621	
1985	AGC	ACT	TTT	AAT	GCT	CCA	GCT	GGA	AAT	GAT	CCT	TTG	GCT	TTA	GAC	TTG	AAT	ACC	ATG	GGC	AAA	GGA	CAA	2053	
622	Ser	Thr	Phe	Phe	Asn	Ala	Pro	Ala	Gly	Asn	Asp	Pro	Leu	Ala	Leu	Asp	Leu	Asn	Thr	Met	Gly	Lys	Gln	644	
2054	GTG	TGG	ATA	AAT	GGT	CAA	AGC	CTC	GGA	CGC	TAT	TGG	CCT	GGA	TAT	AAA	GCA	TCT	GGT	AAC	TGC	GGT	GCC	2122	
645	Val	Trp	Ile	Asn	Gly	Gln	Ser	Leu	Ser	Gly	Arg	Tyr	Trp	Pro	Gly	Tyr	Lys	Ala	Ser	Gly	Asn	Cys	Gly	Ala	667
2123	TGT	AAC	TAT	GCA	GGC	TGG	TTT	AAT	GAG	AAA	AAA	TGC	CTA	AGT	AAC	TGT	GGA	GAG	GCT	TCA	CAA	CGA	TGG	2191	
668	Cys	Asn	Tyr	Ala	Gly	Trp	Phe	Asn	Glu	Lys	Lys	Cys	Leu	Ser	Asn	Cys	Gly	Glu	Ala	Ser	Gln	Arg	Trp	690	
2192	TAT	CAT	GTT	CCC	CGT	TCT	TGG	CTG	TAT	CCT	ACT	GGA	AAT	TTG	TTA	GTT	CTA	TTT	GAG	GAA	TGG	GGA	GGA	2260	
691	Tyr	His	Val	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Leu	Phe	Glu	Glu	Trp	Gly	Gly	713	
2261	GAG	CCT	CAT	GGA	ATC	TCT	TTG	GTA	AAA	AGA	GAA	GTT	GCA	AGT	GTT	TGT	GCA	GAT	ATA	AAC	GAA	TGG	CAA	2329	
714	Glu	Pro	His	Gly	Ile	Ser	Leu	Val	Lys	Arg	Glu	Val	Ala	Ser	Val	Cys	Ala	Asp	Ile	Asn	Glu	Trp	Gln	736	
2330	CCA	CAG	TTG	GTG	AAT	TGG	CAA	ATG	CAA	GCA	TCT	GGT	AAA	GTT	GAC	AAA	CCA	CTG	AGA	CCT	AAA	GCT	CAC	2398	
737	Pro	Gln	Leu	Val	Asn	Trp	Gln	Met	Gln	Ala	Ser	Gly	Lys	Val	Asp	Lys	Pro	Leu	Arg	Pro	Lys	Ala	His	759	
2399	CTC	TCG	TGT	GCT	TCT	GCT	CAG	AAG	ATT	ACT	TCA	ATC	AAA	TTT	GCA	AGC	TTT	GGA	ACA	CCA	CAA	GGG	GTC	2467	
760	Leu	Ser	Cys	Ala	Ser	Gly	Gln	Lys	Ile	Thr	Ser	Ile	Lys	Phe	Ala	Ser	Phe	Gly	Thr	Pro	Gln	Gly	Val	782	
2468	TGC	GGA	AGC	TTC	CGT	GAA	GGA	AGC	TGC	CAC	GCC	TTC	CAC	TCA	TAT	GAT	GCT	TTT	GAA	AGG	TAT	TGC	ATC	2536	
783	Cys	Gly	Ser	Phe	Arg	Glu	Gly	Ser	Cys	His	Ala	Phe	His	Ser	Tyr	Asp	Ala	Phe	Glu	Arg	Tyr	Cys	Ile	805	

FIG. 2C-4

2537	GGG CAA AAC TCG TGC TCA GTA CCT GTA ACA CCA GAG ATC TTT GGA GGT GAT CCA TGT CCA CAT GTT ATG	2605
806	Gly Gln Asn Ser Cys Ser Val Pro Val Thr Pro Glu Ile Phe Gly Gly Asp Pro Cys Pro His Val Met	828
2606	AAG AAA CTC TCA GTT GAG GTT ATT TGC AGT TGA TGACACTGAGGAGAAACAATAAAAGTGGTTTCAGTTAGTTGTCTGAA	2686
829	Lys Lys Leu Ser Val Glu Val Ile Cys Ser ***	840
2687	CATATCAAAAAGTTGGCTTTGATGGAGGTGAAGTTGTACAGATATGCAACACACACCTTTCATTGAGGCACATATGAATTGCAATGGCCCCAA	2778
2779	GATTCTGTACATATATGTTGGTTACTGTCAAGTTGGTATTGGTTGCAAAATGTAAACAGTAGTATAGTCATTGGTTCAAGTGGCATCGAG	2870
2871	ATTGTGCTAGTGGGAGGTAGTAGGTACCGATCGATCTATCGTTGTTGCACAAAGCTGGGCCCTAGATTCCACTATTATTATAACAAGAAAGC	2962
2963	ACAATGAGACTGATTCTTGATTAGTCCCATGTGTAGATATTGTTACTGTGGAATTGCAAAATCTTGTGATTTCAGCAAAAAA	3054
3055	AAAAAAAAAAAAAA	3069

FIG. 2C-5

1	AAAAAAGTTTCAATTTTTTTTCTAAAAATAAAAAAATTCATTTTTTTTGAATGTGAAAAA	63
64	ATG CTA AGG ACT AAT GTG TTG TTA TTA TTA TGT TTA TTG GAT TTT TTT TCT TCA GTG AAA GCT	132
1	Met Leu Arg Thr Asn Val Leu Leu Val Ile Cys Leu Leu Asp Phe Phe Ser Ser Val Lys Ala	23
133	AGT GTT TCT TAT GAT GAC AGA GCT ATA ATC ATA AAT GGG AAA AGA AAA ATT CTT ATT TCT GGT TCA ATT	201
24	Ser Val Ser Tyr Asp Asp Arg Ala Ile Ile Ile Asn Gly Lys Arg Lys Ile Leu Ile Ser Gly Ser Ile	46
202	CAT TAT CCA AGA AGC ACT CCA CAG ATG TGG CCT GAT CTT ATA CAA AAG GCT AAA GAT GGA GGC TTA GAT	270
47	His Tyr Pro Arg Ser Thr Pro Gln Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Asp Gly Leu Asp	69
271	GTT ATT GAA ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT TCT CCT GGA AAA TAT AAT TTT GAA GGA AGA	339
70	Val Ile Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Lys Tyr Asn Phe Glu Gly Arg	92
340	TAT GAT CTT GTT AGA TTC ATC AAA ATG GTA CAA AGA GCA GGA CTT TAT GTC AAT TTA CGT ATT GGC CCT	408
93	Tyr Asp Leu Val Arg Phe Ile Lys Met Val Gln Arg Ala Gly Leu Tyr Val Asn Leu Arg Ile Gly Pro	115

FIG. 2D-1

409	TAC	GTC	TGT	GCT	GAA	TGG	AAC	TTT	GGG	GGA	TTC	CCT	GTT	TGG	CTA	AAA	TAT	GTG	CCT	GGT	ATG	GAA	TTT	477
116	Tyr	Val	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Val	Trp	Leu	Lys	Tyr	Val	Pro	Gly	Met	Glu	Phe	138
478	AGA	ACA	AAC	AAT	CAG	CCT	TTT	AAG	GTG	GCT	ATG	CAA	GGA	TTT	GTT	CAG	AAA	ATA	GTC	AAC	ATG	ATG	AAG	546
139	Arg	Thr	Asn	Asn	Gln	Pro	Phe	Lys	Val	Ala	Met	Gln	Gly	Phe	Val	Gln	Lys	Ile	Val	Asn	Met	Met	Lys	161
547	TCA	GAA	AAT	TTG	TTT	GAA	TCT	CAA	GGA	GGA	CCA	ATA	ATT	ATG	GCC	CAG	ATA	GAA	AAT	GAG	TAT	GGA	CCA	615
162	Ser	Glu	Asn	Leu	Phe	Glu	Ser	Gln	Gly	Gly	Pro	Ile	Ile	Met	Ala	Gln	Ile	Glu	Asn	Glu	Tyr	Gly	Pro	184
616	GTA	GAA	TGG	GAA	ATT	GGT	GCT	GCT	GGT	AAA	GCT	TAT	ACA	AAA	TGG	GCA	GCT	CAA	ATG	GCT	GTA	GGT	TTG	684
185	Val	Glu	Trp	Glu	Ile	Gly	Ala	Pro	Gly	Lys	Ala	Tyr	Thr	Lys	Trp	Ala	Ala	Gln	Met	Ala	Val	Gly	Leu	207
685	AAA	ACT	GGT	GTC	CCA	TGG	ATC	ATG	TGT	AAG	CAA	GAG	GAT	GCT	CCT	GAT	CCT	GTG	ATT	GAT	ACT	TGT	AAT	753
208	Lys	Thr	Gly	Val	Pro	Trp	Ile	Met	Cys	Lys	Gln	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asp	Thr	Cys	Asn	230
754	GGC	TTC	TAC	TGC	GAA	GGG	TTC	CGT	CCT	AAT	AAG	CCT	TAC	AAA	CCT	AAA	ATG	TGG	ACA	GAA	GTA	TGG	ACT	822
231	Gly	Phe	Tyr	Cys	Glu	Gly	Phe	Arg	Pro	Asn	Lys	Pro	Tyr	Lys	Pro	Lys	Met	Trp	Thr	Glu	Val	Trp	Thr	253
823	GGC	TGG	TAT	ACG	AAA	TTC	GGT	GGT	CCA	ATT	CCT	CAA	AGA	CCA	GCC	GAA	GAC	ATT	GCA	TTT	TCA	GTT	GCC	891
254	Gly	Trp	Tyr	Thr	Lys	Phe	Gly	Gly	Pro	Ile	Pro	Gln	Arg	Pro	Ala	Gly	Asp	Ile	Ala	Phe	Ser	Val	Ala	276
892	AGG	TTT	GTT	CAG	AAC	AAT	GGT	TCA	TTC	TTC	AAT	TAC	TAC	ATG	TAT	CAT	GGA	GGA	ACA	AAT	TTT	GGC	CGG	960
277	Arg	Phe	Val	Gln	Asn	Gly	Ser	Phe	Phe	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg		299
961	ACA	TCA	TCA	GGG	CTT	TTC	ATT	GCA	ACT	AGC	TAC	GAT	TAT	GAT	GCT	CCT	CTC	GAT	GAA	TAT	GGG	TTG	CTG	1029
300	Thr	Ser	Ser	Gly	Leu	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr	Gly	Leu	Leu	322

FIG. 2D-2

1030	AAT	GAA	CCA	AAG	TAT	GGG	CAC	TTG	AGA	GAC	TTA	CAT	AAA	GCT	ATC	AAG	CTA	TCT	GAA	CCG	GCT	TTA	GTT	1098
323	Asn	Glu	Pro	Lys	Tyr	Gly	His	Leu	Arg	Asp	Leu	His	Lys	Ala	Ile	Lys	Leu	Ser	Glu	Pro	Ala	Leu	Val	345
1099	TCA	TCA	TAT	GCT	GCG	GTG	ACT	AGT	CTT	GGA	AGT	AAT	CAA	GAG	GCT	CAT	GTT	TAT	AGA	TCA	AAA	TCT	GGA	1167
346	Ser	Ser	Tyr	Ala	Ala	Val	Thr	Ser	Leu	Gly	Ser	Asn	Gln	Glu	Ala	His	Val	Tyr	Arg	Ser	Lys	Ser	Gly	368
1168	GCT	TGT	GCT	GCT	TTT	TTA	TCC	AAC	TAT	GAC	TCT	AGA	TAT	TCA	GTA	AAA	GTC	ACC	TTT	CAG	AAT	AGG	CCA	1236
369	Ala	Cys	Ala	Ala	Phe	Leu	Ser	Asn	Tyr	Asp	Ser	Arg	Tyr	Ser	Val	Lys	Val	Thr	Phe	Gln	Asn	Arg	Pro	391
1237	TAC	AAT	CTG	CCT	CCA	TGG	TCC	ATC	AGC	ATT	CTT	CCC	GAC	TGC	AAA	ACT	GCC	GTT	TAC	AAC	ACT	GCA	CAG	1305
392	Tyr	Asn	Leu	Pro	Pro	Trp	Ser	Ile	Ser	Ile	Leu	Pro	Asp	Cys	Lys	Thr	Ala	Val	Tyr	Asn	Thr	Ala	Gln	414
1306	GTT	AAC	TCT	CAA	AGC	TCG	AGC	ATA	AAG	ATG	ACG	CCT	GCA	GGT	GGT	GGA	TTG	TCT	TGG	CAG	TCA	TAC	AAT	1374
415	Val	Asn	Ser	Gln	Ser	Ser	Ser	Ile	Lys	Met	Thr	Pro	Pro	Ala	Gly	Gly	Leu	Ser	Trp	Gln	Ser	Tyr	Asn	437
1375	GAA	GAA	ACG	CCT	ACT	GCT	GAT	GAC	AGC	GAT	ACA	CTT	ACA	GCT	AAC	GGA	CTA	TGG	GAA	CAG	AAA	AAC	GTC	1443
438	Glu	Glu	Thr	Pro	Thr	Ala	Asp	Ser	Asp	Ser	Thr	Leu	Thr	Ala	Asn	Gly	Leu	Trp	Glu	Gln	Lys	Asn	Val	460
1444	ACA	AGA	GAT	TCA	TCA	GAC	TAT	CTG	TGG	TAC	ATG	ACA	AAT	GTA	AAT	ATA	GCA	TCT	AAT	GAA	GGA	TTT	CTA	1512
461	Thr	Arg	Asp	Ser	Ser	Asp	Tyr	Leu	Trp	Tyr	Met	Thr	Asn	Val	Asn	Ile	Ala	Ser	Asn	Glu	Gly	Phe	Leu	483
1513	AAG	AAC	GGA	AAG	GAT	CCT	TAT	CTC	ACT	GTT	ATG	TCC	GCT	GGT	CAT	GTC	TTG	CAT	GTT	TTC	GTC	AAT	GGA	1581
484	Lys	Asn	Gly	Lys	Asp	Pro	Tyr	Leu	Thr	Val	Met	Ser	Ala	Gly	His	Val	Leu	His	Val	Phe	Val	Asn	Gly	506
1582	AAA	CTA	TCA	GGA	ACT	GTT	TAT	GGT	ACA	TTG	GAT	AAT	CCA	AAA	CTT	ACA	TAC	AGT	GGC	AAC	GTG	AAG	TTA	1650
507	Lys	Leu	Ser	Gly	Thr	Val	Tyr	Gly	Thr	Leu	Asp	Asn	Pro	Lys	Leu	Thr	Tyr	Ser	Gly	Asn	Val	Lys	Leu	529

FIG. 2D-3

1651	AGA	GCT	GGT	ATT	AAC	AAG	ATT	TCT	CTG	CTC	AGT	GTT	TCC	GTT	GGT	CTC	CCG	AAC	GTT	GGC	GTG	CAT	TAT	1719
530	Arg	Ala	Gly	Ile	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Val	Ser	Val	Gly	Leu	Pro	Asn	Val	Gly	Val	His	Tyr	552
1720	GAT	ACA	TGG	AAT	GCA	GGA	GTT	CTA	GGT	CCA	GTC	ACG	TTG	AGC	GGT	CTC	AAT	GAA	GGG	TCA	AGA	AAC	TTG	1788
553	Asp	Thr	Trp	Asn	Ala	Gly	Val	Val	Gly	Pro	Val	Thr	Leu	Ser	Gly	Leu	Asn	Glu	Gly	Ser	Arg	Asn	Leu	575
1789	GCG	AAA	CAG	AAA	TGG	TCT	TAC	AAG	GTT	GGT	CTG	AAA	GGC	GAA	TCG	TTA	AGT	CTT	CAC	TCC	TTA	AGT	GGG	1857
576	Ala	Lys	Gln	Lys	Trp	Ser	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ser	Leu	Ser	Leu	His	Ser	Leu	Ser	Gly	598
1858	AGT	TCT	TCT	GTT	GAA	TGG	GTT	CGA	GGT	TCA	CTA	ATG	GCT	CAA	AAG	CAG	CCC	CTG	ACT	TGG	TAC	AAG	GCT	1926
599	Ser	Ser	Ser	Val	Glu	Trp	Val	Arg	Gly	Ser	Leu	Met	Ala	Gln	Lys	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	Ala	621
1927	ACA	TTT	AAC	GCG	CCT	GGA	GAT	CCA	CTA	GCT	TTA	GAC	ATG	GCA	AGT	ATG	GGA	AAA	GGT	CAG	ATA			1995
622	Thr	Phe	Asn	Ala	Pro	Gly	Gly	Asn	Asp	Pro	Leu	Ala	Leu	Asp	Met	Ala	Ser	Met	Gly	Lys	Gly	Gln	Ile	644
1996	TGG	ATA	AAT	GGT	GAA	GCG	GTA	GGT	CGC	CAT	TGG	CCT	GGA	TAC	ATA	GCA	CAA	GGC	GAC	TGC	AGC	AAA	TGC	2064
645	Trp	Ile	Asn	Gly	Glu	Gly	Val	Gly	Arg	His	Trp	Pro	Gly	Tyr	Ile	Ala	Gln	Gly	Asp	Cys	Ser	Lys	Cys	667
2065	AGT	TAT	GCT	GGA	ACG	TTC	AAC	GAG	AAG	TGC	CAG	ACT	AAC	TGC	GGA	CAA	CCT	TCT	CAG	AGA	TGG	TAC		2133
668	Ser	Tyr	Ala	Gly	Thr	Phe	Asn	Glu	Lys	Lys	Cys	Gln	Thr	Asn	Cys	Gly	Gln	Pro	Ser	Gln	Arg	Trp	Tyr	690
2134	CAT	GTT	CCA	CGA	TCG	TGG	CTG	AAA	CCA	AGT	GGA	AAC	TTG	TTA	GTA	GTA	TTC	GAA	GAA	TGG	GCA	GGT	AAT	2202
691	His	Val	Pro	Arg	Ser	Trp	Leu	Lys	Pro	Ser	Gly	Asn	Leu	Leu	Val	Val	Phe	Glu	Glu	Trp	Gly	Gly	Asn	713
2203	CCA	ACA	GGA	ATT	TCT	CTA	GTC	AGG	AGA	TCA	AGA	TAA	AGAACTCGAA	AAAGTAA	AACTTGTT	CAGTAACT	ATATGGT	GCTTGAA						2282
714	Pro	Thr	Gly	Ile	Ser	Leu	Val	Arg	Arg	Ser	Arg	***												725

FIG. 2D-4

2283	TTCGCGCCGAAAAATACATACACGAAGCTAACAAATGGAGGCTACAGTTTGCAAATTCAGCTGAATAAACATTAGAAGATAAAGAAATATT	2374
2375	TGATTAAAGGAGTATATAAATTACAGAGAAATTTCTTTATTCTTTGTAAAACCTTTGGTTTATAAAGTTTATACAGAAATTTCTCTGTTATTT	2466
2467	GGATTATGAGATTGAAGAAGATTGTACAGCTTCCAATACTATTAGAATACAAATAAATTCATGTAAAAAATAAAAAA	2554

FIG. 2D-5

1	ATC	CAG	ACT	TAC	GTT	TTC	TGG	AAC	CCT	GAT	GAA	CCT	GTT	CGA	AAT	CAG	TAT	GAT	TAT	TTT	GAA	GGA	AGG	AAA	69
1	Ile	Gln	Thr	Tyr	Val	Phe	Trp	Asn	Leu	His	Glu	Pro	Val	Arg	Asn	Gln	Tyr	Asp	Phe	Glu	Gly	Arg	Lys	23	
70	GAT	TTG	ATT	AAT	TTT	GTG	AAG	TTG	GTG	GAG	AGA	GCT	GGC	TTA	TTT	GTT	CAT	ATA	AGG	ATT	GGG	CCT	TAT	138	
24	Asp	Leu	Ile	Asn	Phe	Val	Lys	Leu	Val	Glu	Arg	Ala	Gly	Leu	Phe	Val	His	Ile	Arg	Ile	Gly	Pro	Tyr	46	
139	GTT	TGT	GCA	GAA	TGG	AAC	TAT	GGT	GGG	TTT	CCT	CTT	TGG	TTG	CAT	TTC	ATT	CCT	GGA	ATT	GAA	TTT	CGA	207	
47	Val	Cys	Ala	Glu	Trp	Asn	Tyr	Gly	Gly	Phe	Pro	Leu	Trp	Leu	His	Phe	Ile	Pro	Gly	Ile	Glu	Phe	Arg	69	
208	ACC	GAC	AAT	GAA	CCG	TTC	AAG	GCA	GAA	ATG	AAG	CGA	TTC	ACA	GCT	AAA	ATT	GTT	GAC	ATG	ATC	AAG	CAA	276	
70	Thr	Asp	Asn	Glu	Pro	Phe	Lys	Ala	Glu	Met	Lys	Arg	Phe	Thr	Ala	Lys	Ile	Val	Asp	Met	Ile	Lys	Gln	92	
277	GAA	AAT	CTA	TAT	GCA	TCC	CAG	GGT	GGG	CCG	GTT	ATC	TTG	TCT	CAG	ATA	GAA	AAT	GAG	TAT	GGC	AAT	GGT	345	
93	Glu	Asn	Leu	Tyr	Ala	Ser	Gln	Gly	Gly	Pro	Val	Ile	Leu	Ser	Gln	Ile	Glu	Asn	Glu	Tyr	Gly	Asn	Gly	115	
346	GAT	ATT	GAG	TCT	CGT	TAT	GGT	CCT	CGT	GCC	AAA	CCT	TAC	GTG	AAC	TGG	GCA	GCA	TCA	ATG	GCT	ACG	TCT	414	
116	Asp	Ile	Glu	Ser	Arg	Tyr	Gly	Pro	Arg	Ala	Lys	Pro	Tyr	Val	Asn	Trp	Ala	Ala	Ser	Met	Ala	Thr	Ser	138	
415	TTA	AAT	ACG	GGA	GTG	CCA	TGG	GTT	ATG	TGT	CAG	CAA	CCA	GAT	GCC	CCT	CCT	TCC	GTT	ATT	AAC	ACT	TGC	483	
139	Leu	Asn	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Gln	Gln	Pro	Asp	Ala	Pro	Pro	Ser	Val	Ile	Asn	Thr	Cys	161	
484	AAT	GGA	TTT	TAT	TGT	GAC	CAA	TTC	AAG	CAA	AAT	TCC	GAT	AAA	ACA	CCC	AAG	ATG	TGG	ACT	GAG	AAT	TGG	552	
162	Asn	Gly	Phe	Tyr	Cys	Asp	Gln	Phe	Lys	Gln	Asn	Ser	Asp	Lys	Thr	Pro	Lys	Met	Trp	Thr	Glu	Asn	Trp	184	

FIG. 2E-1

553	ACC	GGA	TGG	TTT	CTG	TCG	TTT	GGT	GGT	CCT	GTC	CCT	TAC	AGA	CCA	GTG	GAA	GAC	ATC	GCT	TTC	GCT	GTG	621
185	Thr	Gly	Trp	Phe	Leu	Ser	Phe	Gly	Gly	Pro	Val	Pro	Tyr	Arg	Pro	Val	Glu	Asp	Ile	Ala	Phe	Ala	Val	207
622	GCT	CGA	TTT	TTC	CAG	CGA	GGC	GGA	ACT	TTC	CAG	AAC	TAT	TAC	ATG	TAC	CAC	GGG	GGA	ACT	AAC	TTT	GGG	690
208	Ala	Arg	Phe	Phe	Gln	Arg	Gly	Gly	Thr	Phe	Gln	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	230
691	AGA	ACC	AGT	GGT	GGA	CCG	TTT	ATT	GCA	ACT	AGC	TAT	GAC	TAT	GAT	GCC	CCT	CTC	GAC	GAA	TAC	GG		755
231	Arg	Thr	Ser	Gly	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr		252	

FIG. 2E-2

1	ATC	CAG	ACA	TAT	GTT	TTT	TGG	AAT	GTT	CAT	GAG	CCT	TCT	CCT	GGC	AAT	TAC	AAT	TTT	GAA	GGA	AGA	TAT	69
1	Ile	Gln	Thr	Tyr	Val	Phe	Trp	Asn	Val	His	Glu	Pro	Ser	Pro	Gly	Asn	Tyr	Asn	Phe	Glu	Gly	Arg	Tyr	23
70	GAC	CTG	GTG	AGG	TTT	GTA	AAA	ACG	ATT	CAG	AAA	GCA	GGG	CTG	TAT	GCT	CAT	CTT	CGA	ATT	GGC	CCT	TAC	138
24	Asp	Leu	Val	Arg	Phe	Val	Lys	Thr	Ile	Gln	Lys	Ala	Gly	Leu	Tyr	Ala	His	Leu	Arg	Ile	Gly	Pro	Tyr	46
139	GTT	TGT	GCA	GAG	TGG	AAT	TTT	GGA	GGG	TTT	CCA	GTA	TGG	CTG	AAG	TAT	GTA	CCT	GGC	ATT	AGC	TTC	AGA	207
47	Val	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Val	Trp	Leu	Lys	Tyr	Val	Pro	Gly	Ile	Ser	Phe	Arg	69
208	GCT	GAT	AAT	GAA	CCT	TTC	AAG	AAC	GCA	ATG	AAA	GGG	TAT	GCT	GAG	AAA	ATT	GTT	AAC	TTG	ATG	AAG	ATC	276
70	Ala	Asp	Asn	Glu	Pro	Phe	Lys	Asn	Ala	Met	Lys	Gly	Tyr	Ala	Glu	Lys	Ile	Val	Asn	Leu	Met	Lys	Ile	92
277	ATA	ATC	TTT	TCG	AGT	CTC	AGG	GTG	GTC	CAA	TCA	TAC	TCT	CAC	AGA	TTG	AGA	ATG	AGT	ATG	GGC	CTC	AAG	345
93	Ile	Ile	Phe	Ser	Ser	Leu	Arg	Val	Val	Gln	Ser	Tyr	Ser	His	Arg	Leu	Arg	Met	Ser	Met	Gly	Leu	Lys	115
346	CCA	AGG	TAC	TTG	GAG	CAC	CGG	GAC	ATC	AGT	ATT	CAA	CAT	GGG	CTG	CAA	ATA	TGG	CAG	TTG	GAT	TTG	AAC	414
116	Pro	Arg	Tyr	Leu	Glu	His	Arg	Asp	Ile	Ser	Ile	Gln	His	Gly	Leu	Gln	Ile	Trp	Gln	Leu	Asp	Leu	Asn	138

FIG. 2F-1

415	ACA	GGC	GTC	CCA	TGG	GTG	ATG	TGC	AAG	GAA	GAT	GCA	CCA	GAT	CCT	GTG	ATC	AAC	ACA	TGC	AAT	GGT	483	
139	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Lys	Glu	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asn	Thr	Cys	Asn	Gly	161
484	TTC	TAC	TGT	GAT	AAT	TTC	TTC	CCA	AAC	AAA	TAC	TAC	AAA	CCT	GCA	ATT	TGG	ACT	GAA	GCT	TGG	AGT	GGA	552
162	Phe	Tyr	Cys	Asp	Asn	Phe	Phe	Pro	Asn	Lys	Pro	Tyr	Lys	Pro	Ala	Ile	Trp	Thr	Glu	Ala	Trp	Ser	Gly	184
553	TGG	TTC	TCG	GAA	TTT	GGC	GGT	CCC	CTT	CAT	CAG	AGA	CCA	GTT	CAG	GAT	TTG	GCA	TTT	GCT	GTT	GCC	CAA	621
185	Trp	Phe	Ser	Glu	Phe	Gly	Gly	Pro	Leu	His	Gln	Arg	Pro	Val	Gln	Asp	Leu	Ala	Phe	Ala	Val	Ala	Gln	207
622	TTT	ATA	CAA	AGA	GGA	GGA	TCT	TTT	GTT	AAC	TAT	TAC	ATG	TAC	CAT	GGG	GGC	ACG	AAC	TTT	GGA	CGC	ACT	690
208	Phe	Ile	Gln	Arg	Gly	Gly	Ser	Phe	Val	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	230
691	GCG	GGT	GGG	CCA	TTC	ATC	ACT	ACC	AGC	TAT	GAT	TAT	GAT	GCC	CCC	CTC	GAC	GAG	TAT	GG				749
231	Ala	Gly	Gly	Pro	Phe	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr					250

FIG. 2F-2

311	CCT CGC AGT GTC CCT GGC CCT TGG ATG GCC CCT GGT CTG GTT CGA TTG CCG AAG GAA GGA GGA GTG GAT GTT ATT	379
70	Pro Arg Ser Val Pro Ala Met Trp Pro Gly Leu Val Arg Leu Ala Lys Glu Gly Val Asp Val Ile	92
380	GAA ACG TAT GTT TTC TGG AAC GGT CAC GAA CCT TCT CCG GGC AAT TAT TAC TTT GGA GGA AGG TTT GAT	448
93	Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Asn Tyr Tyr Phe Gly Gly Arg Phe Asp	115
449	CTA GTC AAA TTT TGT AAG ATC ATT CAG CAG GCT GGA ATG TAT ATG ATT CTT CGG ATT GGA CCA TTT GTA	517
116	Leu Val Lys Phe Cys Lys Ile Ile Gln Gln Ala Gly Met Tyr Met Ile Leu Arg Ile Gly Pro Phe Val	138
518	GCT GCA GAA TGG AAC TTT GGT GGA CTT CCT GGT TGG TTG CAT TAT GTG CCA GGT ACC ACC TTT CGG ACT	586
139	Ala Ala Glu Trp Asn Phe Gly Gly Leu Pro Val Trp Leu His Tyr Val Pro Gly Thr Phe Arg Thr	161
587	GAT AGT GAA CCA TTT AAG TAT CAC ATG CAG AAG TTC ATG ACA TAT ACA GTG AAC TTA ATG AAG AGA GAG	655
162	Asp Ser Glu Pro Phe Lys Tyr His Met Gln Lys Phe Met Thr Tyr Thr Val Asn Leu Met Lys Arg Glu	184
656	AGG CTT TTT GCA TCT CAA GGA GGT CCA ATC ATC TTG TCA CAG GTA GAA AAT GAG TAC GGC TAC TAT GAA	724
185	Arg Leu Phe Ala Ser Gln Gly Gly Pro Ile Ile Leu Ser Gln Val Glu Asn Glu Tyr Gly Tyr Try Glu	207
725	AAT GCA TAT GGA GAA GGA GGG AAA AGG TAT GCC TTA TGG GCT GCT AAA ATG GCC CTT TCT CAA AAT ACT	793
208	Asn Ala Tyr Gly Glu Gly Gly Lys Arg Tyr Ala Leu Trp Ala Ala Lys Met Ala Leu Ser Gln Asn Thr	230
794	GGT GTA CCT TGG ATA ATG TGC CAG CAG TAT GAT GCT CCT GAT CCT GTG ATT GAC ACA TGC AAT TCA TTT	862
231	Gly Val Pro Trp Ile Met Cys Gln Gln Tyr Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn Ser Phe	253
863	TAC TGC GAC CAA TTT AAA CCA ATC TCT CCA AAC AAG CCC AAA ATT TGG ACA GAG AAC TGG CCG GGA TGG	931
254	Tyr Cys Asp Gln Phe Lys Pro Ile Ser Pro Asn Lys Pro Lys Ile Trp Thr Glu Asn Trp Pro Gly Trp	276

FIG. 2G-2

932	TTC	AAG	ACA	TTT	GGG	GCC	AGA	GAT	CCT	CAC	AGG	CCT	GCA	GAA	GAT	GTT	GCT	TAT	TCC	GTG	GCT	CGT	TTT	1000
277	Phe	Lys	Thr	Phe	Gly	Ala	Arg	Asp	Pro	His	Arg	Pro	Ala	Glu	Asp	Val	Ala	Tyr	Ser	Val	Ala	Arg	Phe	299
1001	TTC	CAA	AAA	GGA	AGC	GGA	GTG	CAG	AAT	TAT	TAC	ATG	TAC	CAT	GGT	GGG	ACG	AAC	TTT	GGC	AGG	ACA	GCA	1069
300	Phe	Gln	Lys	Gly	Gly	Ser	Val	Gln	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	Ala	322
1070	GGT	GGC	CCT	TTC	ATT	ACC	ACA	AGT	TAT	GAC	TAT	GAT	GCC	CCA	ATT	GAC	GAA	TAT	GGT	TTA	CCA	AGG	TTT	1138
323	Gly	Gly	Pro	Phe	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Asp	Glu	Tyr	Gly	Leu	Pro	Arg	Phe	345
1139	CCA	AAA	TGG	GGT	CAC	CTT	AAA	GAA	CTT	CAT	AAA	GTC	ATA	AAA	TCG	TGT	GAG	CAT	GCT	CTG	CTG	AAC	AAT	1207
346	Pro	Lys	Trp	Gly	His	Leu	Lys	Glu	Leu	His	Lys	Val	Ile	Lys	Ser	Cys	Glu	His	Ala	Leu	Leu	Asn	Asn	368
1208	GAT	CCA	ACT	CTT	CTT	TCA	TTA	GGT	CCT	CTA	CAA	GAG	GCT	GAT	GTT	TAT	GAA	GAT	GCT	TCA	GGC	GCT	TGT	1276
369	Asp	Pro	Thr	Leu	Leu	Ser	Leu	Gly	Pro	Leu	Gln	Glu	Ala	Asp	Val	Tyr	Glu	Asp	Ala	Ser	Gly	Ala	Cys	391
1277	GCT	GCC	TTT	CTC	GCG	AAT	ATG	GAT	GAC	AAA	AAT	GAC	AAG	GTG	GTA	CAG	TTC	CGA	CAT	GTA	TCA	TAC	CAC	1345
392	Ala	Ala	Phe	Leu	Ala	Asn	Met	Asp	Asp	Lys	Asn	Asp	Lys	Val	Val	Gln	Phe	Arg	His	Val	Ser	Tyr	His	414
1346	TTG	CCA	GCA	TGG	TCT	GTT	AGC	ATT	TTG	CCA	GAC	TGC	AAA	AAT	GTA	GCG	TTC	AAC	ACA	GCA	AAG	GTT	GGA	1414
415	Leu	Pro	Ala	Trp	Ser	Val	Ser	Ile	Leu	Pro	Pro	Asp	Cys	Lys	Asn	Val	Ala	Phe	Asn	Thr	Ala	Lys	Gly	437
1415	TGT	CAA	ACT	TCT	ATT	GTC	AAT	ATG	GCA	CCC	ATA	GAT	TTG	CAT	CCC	ACC	GCA	AGT	TCA	CCA	AAG	AGA	GAC	1483
438	Cys	Gln	Thr	Ser	Ile	Val	Asn	Met	Ala	Pro	Ile	Asp	Leu	His	Pro	Thr	Ala	Ser	Ser	Pro	Lys	Arg	Asp	460
1484	ATC	AAG	TCT	CTT	CAG	TGG	GAA	GTC	TTC	AAG	GAA	ACA	GCT	GGA	GTA	TGG	GGA	GTT	GCT	GAT	TTC	ACT	AAA	1552
461	Ile	Lys	Ser	Leu	Gln	Trp	Glu	Val	Phe	Lys	Glu	Thr	Ala	Gly	Val	Trp	Gly	Val	Ala	Asp	Phe	Thr	Lys	483

FIG. 2G-3

1553	AAC	GGA	TTT	GTA	GAT	CAC	ATT	AAC	ACC	ACA	AAA	GAT	GCT	ACA	GAC	TAC	TGG	CTC	TGG	TAC	ACA	ACA	AGT	ATT	1621
484	Asn	Gly	Phe	Val	Asp	His	Ile	Asn	Thr	Thr	Lys	Asp	Ala	Thr	Asp	Tyr	Leu	Trp	Tyr	Thr	Thr	Ser	Ile	506	
1622	TTT	GTT	CAT	GCA	GAG	GAG	GAT	TTC	CTA	AGA	AAC	AGA	GGC	ACT	GCA	ATG	CTT	TTC	GTT	GAA	TCA	AAG	GGT	1690	
507	Phe	Val	His	Ala	Glu	Glu	Asp	Phe	Leu	Arg	Asn	Arg	Gly	Thr	Ala	Met	Leu	Phe	Val	Glu	Ser	Lys	Gly	529	
1691	CAT	GCT	ATG	CAT	GTC	TTC	ATC	AAT	AAA	AAG	CTT	CAA	GCC	AGT	GCA	TCT	GGA	AAT	GGC	ACA	GTG	CCA	CAG	1759	
530	His	Ala	Met	His	Val	Phe	Ile	Asn	Lys	Lys	Leu	Gln	Ala	Ser	Ala	Ser	Gly	Asn	Gly	Thr	Val	Pro	Gln	552	
1760	TTC	AAG	TTT	GGA	ACT	CCT	ATT	GCT	CTA	AAG	GCA	GGG	AAG	AAT	GAA	ATT	TCC	TTG	TTA	AGC	ATG	ACT	GTG	1828	
553	Phe	Lys	Phe	Gly	Thr	Pro	Ile	Ala	Leu	Lys	Ala	Gly	Lys	Asn	Glu	Ile	Ser	Leu	Leu	Ser	Met	Thr	Val	575	
1829	GGC	CTA	CAA	ACA	GCT	GGA	GCG	TTT	TAT	GAA	TGG	ATT	GGA	GCT	GGT	CCA	ACA	AGT	GTC	AAA	GTT	GCA	GGG	1897	
576	Gly	Leu	Gln	Thr	Ala	Gly	Ala	Phe	Tyr	Glu	Trp	Ile	Gly	Ala	Gly	Pro	Thr	Ser	Val	Lys	Val	Ala	Gly	598	
1898	TTC	AAG	ACT	GGG	ACT	ATG	GAC	TTG	ACT	GCG	TCT	GCT	TGG	ACC	TAT	AAG	ATT	GGA	TTG	CAA	GGA	GAA	CAT	1966	
599	Phe	Lys	Thr	Gly	Thr	Met	Asp	Leu	Thr	Ala	Ser	Ala	Trp	Thr	Tyr	Lys	Ile	Gly	Leu	Gln	Gly	Glu	His	621	
1967	TTG	AGG	ATA	CAG	AAG	TCA	TAT	AAC	TTG	AAG	AGT	AAA	ATT	TGG	GCA	CCA	ACT	TCG	CAG	CCA	CCA	AAG	CAA	2035	
622	Leu	Arg	Ile	Gln	Lys	Ser	Tyr	Asn	Leu	Lys	Ser	Lys	Ile	Trp	Ala	Pro	Thr	Ser	Gln	Pro	Pro	Lys	Gln	644	
2036	CAG	CCC	CTC	ACA	TGG	TAT	AAG	GCA	GTA	GTA	GAT	GCG	CCT	CCT	GGT	AAT	GAA	CCT	GTT	GCA	CTT	GAT	ATG	2104	
645	Gln	Pro	Leu	Thr	Thr	Trp	Tyr	Lys	Ala	Val	Val	Asp	Ala	Pro	Gly	Asn	Glu	Pro	Val	Ala	Leu	Asp	Met	667	
2105	ATT	CAT	ATG	GGA	AAA	GGA	ATG	GCT	TGG	TTG	AAT	GGA	CAA	GAA	ATT	GGC	AGA	TAT	TGG	CCG	AGG	AGA	ACT	2173	
668	Ile	His	Met	Gly	Lys	Gly	Met	Ala	Trp	Leu	Asn	Gly	Gln	Glu	Ile	Gly	Art	Tyr	Trp	Pro	Arg	Arg	Thr	690	

FIG. 2G-4

2174	TCT AAA TAT GAG AAT TGT GTT ACT CAA TGT GAC TAC AGA GGC AAA TTT AAC CCT GAT AAG TGT GTC ACT	2242
691	Ser Lys Tyr Tyr Glu Asn Cys Val Thr Gln Cys Asp Tyr Arg Gly Lys Phe Asn Pro Asp Lys Cys Val Thr	713
2243	GGC TGT GGA CAA CCT ACA CAG AGA TGG TAT CAT GTG CCA CGA TCT TGG TTC AAG CCA TCA GGA AAT GTC	2311
714	Gly Cys Gly Gln Pro Thr Gln Arg Trp Tyr His Val Pro Arg Ser Trp Phe Lys Pro Ser Gly Asn Val	736
2312	TTA ATT ATC TTT GAG GAA ATA GGT GGA GAT CCC TCT CAA ATT AGA TTC TCA ATG CGA AAG GTT TCT GGA	2380
737	Leu Ile Ile Phe Glu Glu Ile Gly Gly Asp Pro Ser Gln Ile Arg Phe Ser Met Arg Lys Val Ser Gly	759
2381	GCT TGT GGT CAT CTT TCA GTG GAC CAT CCA TCC TTT GAT GTT GAA AAT CTG CAA GGA AGT GAA ATT GAG	2449
760	Ala Cys Gly His Leu Ser Val Asp His Pro Ser Phe Asp Val Glu Asn Leu Gln Gly Ser Glu Ile Glu	782
2450	AAC GAC AAA AAC AGG CCA ACT CTA AGT TTG AAA TGC CCC ACA AAT ACT AAT TCC TCT GTC AAA TTT	2518
783	Asn Asp Lys Asn Arg Pro Thr Leu Ser Leu Lys Cys Pro Thr Asn Thr Asn Ile Ser Ser Val Lys Phe	805
2519	GCC AGC TTT GGA AAT CCT AAT GGT ACA TGT GGT TCC TAC ATG CTA GGA GAC TGC CAC GAT CAG AAT TCT	2587
806	Ala Ser Phe Gly Asn Pro Asn Gly Thr Cys Gly Ser Tyr Met Leu Gly Asp Cys His Asp Gln Asn Ser	828
2588	GCA GCA CTG GTC GAA AAG GTT TGC CTG AAC CAA AAT GAG TGT GCA TTA GAA ATG TCC AGC GCA AAC TTT	2656
829	Ala Ala Leu Val Glu Lys Val Cys Leu Asn Gln Asn Glu Cys Ala Leu Glu Met Ser Ser Ala Asn Phe	851
2657	AAC ATG CAA TTG TGT CCA AGT ACA GTA AAG AAA CTT GCA GTT GAA GTG AAT TGC AGC TGA GTGTCATTGCC	2728
852	Asn Met Gln Leu Cys Pro Ser Thr Val Lys Lys Leu Ala Val Glu Val Asn Cys Ser ***	871
2729	AAAATGAATGACATATTCTAATTTATATAGTTTGTACGGAGATGCTCATTCTTAAACCTTTCTTATATAGCAGAAAAATCTGCTATTCCTT	2820
2821	CTTTCGCTATGATTGAAGTTTAAGAFATGAGTACTGATGTCTTATTAAAGCATCACCAGATAACCTTGGATATTCATGTTTGAAAGACTAA	2912
2913	GTATTCATATTTATTCAGTCGAGATGCAAGATTTATTGTGAAAAAATAAAAAA	2972

FIG. 2G-5

		10	20	30	40	50	
TBG1-ORF	-24MGFWMA	MLLMLLCLW	VSCGISVSYD	26
TBG2-ORF	-14MSRRKT	LNFPILITVL	TIHFVI VAGE	YFKPFNVTYD	36
TBG3-ORF	-20	MGCTLI LMLN	VLLVLLGSWV	FSGTASVSYD	30
TBG4-ORF	-22MLRTNVLL	LLVICLLDFF	SSVKASVSYD	28
TBG5-ORF	1	-----	-----	-----	-----	-----	50
TBG6-ORF	1	-----	-----	-----	-----	-----	50
TBG7-ORF	-1	.MNTMSCLS	NFKFVFLAST	VIWMTVMSS	LAAVDASNVT	TIGTDSVTYD	49
apple	-21MGVGIQTMW	SILLLFSCIF	SAASASVSYD	29
carnation	-16MLCG	KENNVMMKML	VYVFVLITLI	SCVYGNVWYD	34
asparagus	-20	MALKVLMLM	VALLAAVWSP	PAVTASVTYD	30
broccoli	-20	MKMKQFNLLS	LFLILITSEF	SANSTIVSHD	30
Lupin	-12MFGSRI VM	ESLMSRRNFH	MVLLLLFFWV	CYVTASVTYD	38
		60	70	80	90	100	
TBG1-ORF	27	HKAIIVNGQR	KILISGSIHY	PRSTPEMWP	LIQKAKEGGV	DVIQTYVFWN	76
TBG2-ORF	37	NRALIIGGKR	RMLISAGIHY	PRATPEMWPT	LIARSKEGGA	DVIETYTFWN	86
TBG3-ORF	31	HRAIIVNGQR	RILISGSVHY	PRSTPEMWPG	IIQKAKEGGV	DVIQTYVFWN	80
TBG4-ORF	29	DRAIINGKR	KILISGSIHY	PRSTPQMWP	LIQKAKDGGL	DVIETYVFWN	78
TBG5-ORF	51	-----	-----	-----	-----	--IQTYVFWN	100
TBG6-ORF	51	-----	-----	-----	-----	--IQTYVFWN	100
TBG7-ORF	50	RRSLIINGQR	KLLISASIHY	PRSVPMWPG	LVRlakeggv	DVIETYVFWN	99
apple	30	HKAIINGQK	RILISGSIHY	PRSTPEMWP	LIQKAKDGGL	DVIQTYVFWN	79
carnation	35	YRAIKINDQR	RILLSGSIHY	PRSTPEMWP	IEKAKDSQL	DVIQTYVFWN	84
asparagus	31	HKSVIINGQR	RILISGSIHY	PRSTPEMWP	LIQKAKDGGL	DVIQTYVFWN	80
broccoli	31	ERAITIDGQR	RILLSGSIHY	PRSTDMMWP	LISKAKDGGL	DTIETYVFWN	80
Lupin	39	HKAIMINGQR	RILISGSIHY	PRSTPQMWP	LIQKAKDGGL	DVIETYVFWN	88
		110	120	130	140	150	
TBG1-ORF	77	GHEPEEGKYY	FEERYDLVKF	IKVVQEAGLY	VHLRIGPYAC	AEWNFGGFPV	126
TBG2-ORF	87	GHEPTRGQYN	FEGRYDVKF	AKLVGSHGLF	LFI RIGPYAC	AEWNFGGFPV	136
TBG3-ORF	81	GHEPQQGKYY	FEGRYDLVKF	IKLVHQAGLY	VHLRVGPYAC	AEWNFGGFPV	130
TBG4-ORF	79	GHEPSPGKYN	FEGRYDLVRF	IKMVQRAGLY	VNLRIGPYVC	AEWNFGGFPV	128
TBG5-ORF	101	LHEPVRNQYD	FEGRKDLINF	VKLVERAGLF	VHIRIGPYVC	AEWNYGGFPL	150
TBG6-ORF	101	VHEPSPGNYN	FEGRYDLVRF	VKTIQKAGLY	AHLRIGPYVC	AEWNFGGFPV	150
TBG7-ORF	100	GHEPSPGNYY	FGGRFDLVKF	CKIIQQAGMY	MLRIGPFVA	AEWNFGGLPV	149
apple	80	GHEPSPGNYY	FEERYDLVKF	IKLVQQEGLF	VNLRIGPYVC	AEWNFGGFPV	129
carnation	85	GHEPSEGKYY	FEGRYDLVKF	IKLIHQAGLF	VHLRIGPFAC	AEWNFGGFPV	134
asparagus	81	GHEPSPGQYY	FGGRYDLVRF	LKLVKQAGLY	AHLRIGPYVC	AEWNFGGFPV	130
broccoli	81	AHEPSRRQYD	FSGNLDLVRF	IKTIQSAGLY	SVLRIGPYVC	AEWNYGGFPV	130
Lupin	89	GHEPSPGKYY	FEDRFDLVGF	IKLVQQAGLF	VHLRIGPFIC	AEWNFGGFPV	138

FIG. 3A

		160	170	180	190	200	
TBG1-ORF	127	WLKYVPGISF	RTNNEPFKAA	MQKFTTKI VD	MMK-----AE	KLYETQGGPI	176
TBG2-ORF	137	WLRDIPGIEF	RTDNAPFKEE	MERYVKKI VD	LMI-----SE	SLFSWQGGPI	186
TBG3-ORF	131	WLKYVPGISF	RTDNGPFKAA	MQKFTAKI VN	MMK-----AE	RLYETQGGPI	180
TBG4-ORF	129	WLKYVPGMEF	RTNNQPFKVA	MQGFVQKI VN	MMK-----SE	NLFESQGGPI	178
TBG5-ORF	151	WLHFIPGIEF	RTDNEPFKAE	MKRFTAKI VD	MIK-----QE	NLYASQGGPV	200
TBG6-ORF	151	WLKYVPGISF	RADNEPFKNA	MKGyAEKI VN	LMKIIIFSSL	RVVQSYSHRL	200
TBG7-ORF	150	WLHYVPGTTF	RTDSEPFKYH	MQKFMTYTVN	LMK-----RE	RLFASQGGPI	199
apple	130	WLKYVPGIAF	RTDNEPFKAA	MQKFTEKI VS	MMK-----AE	KLFQTQGGPI	179
carnation	135	WLKYVPGIEF	RTDNGPFKEK	MQVFTTKI VD	MMK-----AE	KLFHWQGGPI	184
asparagus	131	WLKYVPGIHF	RTDNGPFKAA	MKGfTEKI VS	MMK-----AE	GLYETQGGPI	180
broccoli	131	WLHNMPDMKF	RTINPGFMNE	MQNFTTKI VN	MMK-----EE	SLFASQGGPI	180
Lupin	139	WLKYVPGIAF	RTDNEPFKEA	MQKFTEKI VN	IMK-----AE	KLFQSQGGPI	188
		210	220	230	240	250	
TBG1-ORF	177	ILSQ-IENEY	GP--MEWELG	EPGKVYSEWA	AKMAVDLGTG	VPWIMCKQD-	226
TBG2-ORF	187	ILLQ-IENEY	GN--VESSFG	PKGKLYMKWA	AEMAVGLGAG	VPWVMCRQ-T	236
TBG3-ORF	181	ILSQ-IENEY	GP--MEWELG	APGKSYAQWA	AKMAVGLDTG	VPWVMCKQD-	230
TBG4-ORF	179	IMAQ-IENEY	GP--VEWEIG	APGKAYTKWA	AQMAVGLKTG	VPWIMCKQE-	228
TBG5-ORF	201	ILSQ-IENEY	GNGDIESRYG	PRAKPYVNWA	ASMATSLNTG	VPWVMCQQ-P	250
TBG6-ORF	201	RMSMGLKPRY	----LEHRDI	SIQHGLQIWQ	----LDLNTG	VPWVMCKEE-	250
TBG7-ORF	200	ILSQ-VENEY	G--YYENAYG	EGGKRYALWA	AKMALSQNTG	VPWIMC-QQY	249
apple	180	ILSQ-IENEF	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	VPWIMCKQE-	229
carnation	185	ILNQ-IENEY	GP--VEWEIG	APGKAYTHWA	AQMAQSLNAG	VPWIMCKQDS	234
asparagus	181	ILSQ-IENEY	GP--VEYYDG	AAGKSYTNWA	AKMAVGLNTG	VPWVMCKQD-	230
broccoli	181	ILAQ-IENEY	GN--VISSYG	AEGKAYIDWC	ANMANSLDIG	VPWIMC-QQP	230
Lupin	189	ILSQ-IENEY	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	VPWVMCKQE-	238
		260	270	280	290	300	
TBG1-ORF	227	DVPDPIINTC	NGFYCDYFTP	NKANKPKMWT	EAWTAWFTEF	GGPVPYRP AE	276
TBG2-ORF	237	DAPEYIIDTC	NAYYCDGFTP	NSEKKPKI WT	ENWNGWFADW	GERLPYRPSE	286
TBG3-ORF	231	DAPDPIINAC	NGFYCDYFSP	NKAYKPKI WT	EAWTAWFTGF	GNPVPYRP AE	280
TBG4-ORF	229	DAPDPVIDTC	NGFYCEGFRP	NKPYKPKMWT	EVWTGWYTKF	GGPI PQRP AE	278
TBG5-ORF	251	DAPPSVINTC	NGFYCDQFKQ	NSDKTPKMWT	ENWTGWFLSF	GGPVPYRP VE	300
TBG6-ORF	251	DAPDPVINTC	NGFYCDNFFP	NKPYKPAI WT	EAWSGWFSEF	GGPLHQRPVQ	300
TBG7-ORF	250	DAPDPVIDTC	NSFYCDQFKP	ISPNKPKI WT	ENWPGWFKTF	GARDPHRP AE	299
apple	230	DAPDPVIDTC	NGFYCENFKP	NKDYKPKMWT	EVWTGWYTEF	GGAVPTRP AE	279
carnation	235	DVPDNVIDTC	NGFYCEGFVP	KDKSKPKMWT	ENWTGWYTEY	GKPPYRP AE	284
asparagus	231	DAPDPVINTC	NGFYCDYFSP	NKDNKPKMWT	EAWTGWFTGF	GGAVPQRP AE	280
broccoli	231	HAPQPMIETC	NGFYCDQYKP	SNPSSPKMWT	ENWTGWFKNW	GKGHPYRTAE	280
Lupin	239	DAPDPIIDTC	NGFYCENFTP	NKNYKPKLWT	ENWTGWYTAF	GGATPYRP AE	288

FIG. 3B

		310	320	330	340	350	
TBG1-ORF	277	DMAFAVARFI	QTGGSFINYY	MYHGGETNFGR	TSGGPFIATS	YDYDAPLDEF	326
TBG2-ORF	287	DI AF AI ARFF	QRGGS LQ NY Y	MYFGGTNFGR	TAGGP TQ ITS	YDYDAPLDEY	336
TBG3-ORF	281	DLAFSVAKFI	QKGGSF INYY	MYHGGETNFGR	TAGGPFIATS	YDYDAPLDEY	330
TBG4-ORF	279	DI AF SVARFV	QNNGSFFNY Y	MYHGGETNFGR	TSSGLFIATS	YDYDAPLDEY	328
TBG5-ORF	301	DI AF AVARFF	QRGGTFQ NY Y	MYHGGETNFGR	TSGGPFIATS	YDYDAPLDEY	350
TBG6-ORF	301	DLAFAVAQFI	QRGGSFV NY Y	MYHGGETNFGR	TAGGPFI TTS	YDYDAPLDEY	350
TBG7-ORF	300	DVAYSVARFF	QKGGSVQ NY Y	MYHGGETNFGR	TAGGPFI TTS	YDYDAPI DEY	349
apple	280	DVAFSVARFI	QSGGSFL NY Y	MYHGGETNFGR	TAGGPFMATS	YDYDAPLDEY	329
carnation	285	DVAFSVARFI	QNNGSFM NY Y	MFHGGETNFE-	TTAGRFVSTS	YDYDAPLDEY	334
asparagus	281	DMAFAVARFI	QKGGSF INYY	MYHGGETNFGR	TAGGPFI STS	YDYDAPI DEY	330
broccoli	281	DLAFSVARFF	QTGGTFQ NY Y	MYHGGETNFGR	VAGGPYI TTS	YDYDAPLDEY	330
Lupin	289	DI AF SVARFI	QNRGSLF NY Y	MYHGGETNFGR	TSNGLFVATS	YDYDAPI DEY	338
		360	370	380	390	400	
TBG1-ORF	327	GSLRQPKWGH	LKDLHRAI KL	CEPALVSVD-	PTVTS LG NY Q	EARVFKSES-	376
TBG2-ORF	337	GLLRQPKWGH	LKDLHAAI KL	CEPALVAADS	PQYI KL GP KQ	EAHVYRGT SN	386
TBG3-ORF	331	GLLRQPKWGH	LKDLHRAI KL	CEPALVSGD-	PAVTALGHQ Q	EAHVFRSKA-	380
TBG4-ORF	329	GLLNEPKYGH	LRDLHKAI KL	SEPALVSSY-	AAVTS LG SN Q	EAHVYRSKS-	378
TBG5-ORF	351	-----	-----	-----	-----	-----	400
TBG6-ORF	351	-----	-----	-----	-----	-----	400
TBG7-ORF	350	GLPRFPKWGH	LKELHKVI KS	CEHALLNND-	PTLLSLG PLQ	EADVYEDAS-	399
apple	330	GLPREPKWGH	LRDLHKAI KS	CESALVSVD-	PSVTKLGS NQ	EAHVFKSES-	379
carnation	335	GLPREPKYTH	LKNLHKAI KM	CEPALVSSD-	AKVTNLGS NQ	EAHVYSSNS-	384
asparagus	331	GLLRQPKWGH	LRDLHKAI KL	CEPALVSGE-	PTITS LG Q NQ	ESYVYRSKS-	380
broccoli	331	GNLNQPKWGH	LKQLHTLLKS	MEKPLTYGNI	STID-LGNSV	TATVYSTNEK	380
Lupin	339	GLLNEPKWGH	LRELHRAI KQ	CESALVSVD-	PTVSWPGKNL	EVHLYKTES-	388
		410	420	430	440	450	
TBG1-ORF	377	-----	GACAAFLANY	NQHSFAK VAF	GNMHYNLPPW	SISILPDCKN	426
TBG2-ORF	387	NIGQYMSLNE	GICAAFI ANI	DEHESATVKF	YGQEFTLPPW	SVVF---CQI	436
TBG3-ORF	381	-----	GSCAAFLANY	DQHSFATVSF	ANRHYNLPPW	SISILPDCKN	430
TBG4-ORF	379	-----	GACAAFLS NY	DSRYSVKVTF	QNRPYNLPPW	SISILPDCKT	428
TBG5-ORF	401	-----	-----	-----	-----	-----	450
TBG6-ORF	401	-----	-----	-----	-----	-----	450
TBG7-ORF	400	-----	GACAAFLANM	DDKNDKV VQF	RHVSYHLP AW	SVSILPDCKN	449
apple	380	-----	D-CAAF LANY	DAKYSVKVSF	GGGQYDLPPW	SISILPDCKT	429
carnation	385	-----	GSCAAFLANY	DPKWSVKVTF	SGMEFELPAW	SISILPDCKK	434
asparagus	381	-----	-SCAAFLANF	NSRYYATVTF	NGMHYNLPPW	SVSILPDCKT	430
broccoli	381	S-----	-SC--FIGNV	NATADALVNF	KGKDYNVPAW	SVSVLPDCDK	430
Lupin	389	-----	A-CAAF LANY	NTDYSTQVKF	GNGQYDLPPW	SISILPDCKT	438

FIG. 3C

		460	470	480	490	500	
TBG1-ORF	427	TVYNTARVGA	QSAQM--K--	-----	-----MTP	VSRGFS--WE	476
TBG2-ORF	437	AEIQLSTQLR	WGHKLQSKQW	AQILFQLGII	LCFYKLSLKA	SSESFSQSWM	486
TBG3-ORF	431	TVFNTARIGA	QSAQM--K--	-----	-----MTP	VSRGLP--WQ	480
TBG4-ORF	429	AVYNTAQVNS	QSSSI--K--	-----	-----MTP	AGGGLS--WQ	478
TBG5-ORF	451	-----	-----	-----	-----	-----	500
TBG6-ORF	451	-----	-----	-----	-----	-----	500
TBG7-ORF	450	VAFNTAKVGC	QTSI VNMAP-	-----ID	L--HPTASSP	KRDIKSLQWE	499
apple	430	EVYNTAKVGS	QSSQV--Q--	-----	-----MTP	VHSGFP--WQ	479
carnation	435	EVYNTARVNE	PSPKLHSK--	-----	-----MTP	VISNLN--WQ	484
asparagus	431	TVFNTARVGA	QTTM--K--	-----	-----MQY	LG-GFS--WK	480
broccoli	431	EAYNTARVNT	QTSIITEDS-	-----	-C-----D	EPEKCLKWTR	480
Lupin	439	EVFNTAKVNS	PRLHR--K--	-----	-----MTP	VNSAFA--WQ	488
		510	520	530	540	550	
TBG1-ORF	477	S-FNEDAASH	EDD-TFTVVG	LLEQINI TRD	VSDYLWYMTD	IEIDPTE-GF	526
TBG2-ORF	487	T-LKEPLGVW	GDKN-FTSKG	I LEHLNVTKD	QSDYLWYLTR	IYISDDDISF	536
TBG3-ORF	481	S-FNEETSSY	EDS-SFTVVG	LLEQINTTRD	VSDYLWYSTD	VKIDSRE-KF	530
TBG4-ORF	479	S-YNEETPTA	DDSDTLTANG	LWEQKNVTRD	SSDYLWYMTN	VNI ASNE-GF	528
TBG5-ORF	501	-----	-----	-----	-----	-----	550
TBG6-ORF	501	-----	-----	-----	-----	-----	550
TBG7-ORF	500	V-FKETAGVW	GVAD-FTKNG	FVDHINTTKD	ATDYLWYTTS	IFVHAEF-DF	549
apple	480	S-FIEETTSS	DETDTTTLDG	LYEQINI TRD	TTDYLWYMTD	ITIGSDE-AF	529
carnation	485	S-YSDEVPTA	DSPGTFREKK	LYEQINMTWD	KSDYLWYMTD	VVL D GNE-GF	534
asparagus	481	A-YTEDTDAL	NDN-TFTKDG	LVEQLSTTWD	RSDYLWYTTY	VDI AKNE-EF	530
broccoli	481	PEFTTQKTIL	KGSGDLIAKG	LVDQKDV TND	ASDYLWYMTD	VHL D KKDPIW	530
Lupin	489	S-YNEEPASS	SENDPVTGYA	LWEQVGVT RD	SSDYLWYLT D	VNI GPND---	538
		560	570	580	590	600	
TBG1-ORF	527	LNSGN-WPWL	TVFSAGHALH	VFVNGQLAGT	VYGSLNP KL	TFSNGINLRA	576
TBG2-ORF	537	WEENDVSPTI	DIDSMRDFVR	IFVNGQLAGS	VKGKW----I	KVVQPVKLVQ	586
TBG3-ORF	531	LRGGK-WPWL	TIMSAGHALH	VFVNGQLAGT	AYGSLEKPKL	TFSKAVNLRA	580
TBG4-ORF	529	LKNGK-DPYL	TVMSAGHVLH	VFVNGKLSGT	VYGTLDNP KL	TYSGNVKLRA	578
TBG5-ORF	551	-----	-----	-----	-----	-----	600
TBG6-ORF	551	-----	-----	-----	-----	-----	600
TBG7-ORF	550	LRN-RGTAML	FVESKGHAMH	VFINKKLQAS	ASGNGTVPQF	KFGTPI ALKA	599
apple	530	LKNGK-SPLL	TIFSAGHALN	VFINGQLSGT	VYGSLNP KL	SFSQNVNLRS	579
carnation	535	LKKGD-EPWL	TVNSAGHVLH	VFVNGQLQGH	AYGSLAKPQL	TFSQKVKMTA	584
asparagus	531	LKTGK-YPYL	TVMSAGHAVH	VFINGQLSGT	AYGSLDNP KL	TYSGSAKLWA	580
broccoli	531	SRNMS----L	RVHSHNAVLH	AYVNGKYVGN	QIVRDNKF DY	RFEKKVNLVH	580
Lupin	539	IKDGK-WPVL	TAMSAGHVLN	VFINGQYAGT	AYGSLDDPRL	TFSQSVNL RV	588

FIG. 3D

		610	620	630	640	650	
TBG1-ORF	577	GVNKISLLSI	AVGLPNVGP	FETWNAGVLG	PVSLNGLNEG	T---RDLTWQ	626
TBG2-ORF	587	GYNDILLSE	TVGLQNYGAF	LEKDGAGFKG	QIKLTGCKSG	D---INLTTS	636
TBG3-ORF	581	GVNKISLLSI	AVGLPNIGPH	FETWNAGVLG	PVSLTGLDEG	K---RDLTWQ	630
TBG4-ORF	579	GINKISLLSV	SVGLPNVGVH	YDTWNAGVLG	PVTLSGLNEG	S---RNLAKQ	628
TBG5-ORF	601	-----	-----	-----	-----	-----	650
TBG6-ORF	601	-----	-----	-----	-----	-----	650
TBG7-ORF	600	GKNEISLLSM	TVGLQTAGAF	YE-WIGAGPT	SVKVAGFKTG	T---MDLTAS	649
apple	580	GINKLALLSI	SVGLPNVGTH	FETWNAGVLG	PITLKGLNSG	T---WMSGW	629
carnation	585	GVNRISLLSA	VVGLANVGWH	FERYNQGVLG	PVTLSGLNEG	T---RDLTWQ	634
asparagus	581	GSNKISILSV	SVGLPNVGNH	FETWNTGVLG	PVTLTGLNEG	K---RDLTLQ	630
broccoli	581	GTNHLALLSV	SVGLQNYGPF	FESGPTGING	PVKLVGYKGD	ETIEKDLSKH	630
Lupin	589	GNNKISLLSV	SVGLANVGTH	FETWNTGVLG	PVTLTGLSSG	T---WDL SKQ	638
		660	670	680	690	700	
TBG1-ORF	627	KWFKYVGLKG	EALSLHSLSG	SPSVE--WVE	GSLVAQKQPL	SWYKTTFNAP	676
TBG2-ORF	637	LWTYQVGLRG	EFLEVYDVNS	TESAG--WTE	FPTGTTPSVF	SWYKTKFDAP	686
TBG3-ORF	631	KWSYKVGLKG	EALSLHSLSG	SSSVE--WVE	GSLVAQRQPL	TWYKSTFNAP	680
TBG4-ORF	629	KWSYKVGLKG	ESLSLHSLSG	SSSVE--WVR	GSLMAQKQPL	TWYKATFNAP	678
TBG5-ORF	651	-----	-----	-----	-----	-----	700
TBG6-ORF	651	-----	-----	-----	-----	-----	700
TBG7-ORF	650	AWTYKIGLQG	EHLRIQKSYN	LKSKI--WAP	TSQPPKQQPL	TWYKAVVDAP	699
apple	630	KWTYKTGLKG	EALGLHTVTG	SSSVE--WVE	GPSMAEKQPL	TWYKATFNAP	679
carnation	635	YWSYKIGTKG	EEQQVYNSGG	SSHVQ--WGP	PAW---KQPL	VWYKTTFDAP	684
asparagus	631	KWTYQIGLHG	ETLSLHSLTG	SSNVE--WGE	AS---QKQPL	TWYKTTFNAP	680
broccoli	631	QWDYKIGLNG	FNHKLFSMKS	AGHHHRKWST	EKLPA DRM-L	SWYKANFKAP	680
Lupin	639	KWSYKIGLKG	ESLSLHTEAG	SNSVE--WVQ	GSLVAKKQPL	AWYKTTFSAP	688
		710	720	730	740	750	
TBG1-ORF	677	DGNEPLALDM	NTMGKGQVWI	NGQSLGRHWP	AYKSS-GSCS	V-CNYTGWFD	726
TBG2-ORF	687	GGTDPVALDF	SSMGKGQAWV	NGHHVGRYWT	LVAPN-NGCG	RTCDYRGAYH	736
TBG3-ORF	681	AGNDPLALDL	NTMGKGQVWI	NGQSLGRYWP	GYKAS-GNCG	A-CNYAGWFN	730
TBG4-ORF	679	GGNDPLALDM	ASMKGQIWI	NGEGVGRHWP	GYIAQ-GDCS	K-CSYAGTFN	728
TBG5-ORF	701	-----	-----	-----	-----	-----	750
TBG6-ORF	701	-----	-----	-----	-----	-----	750
TBG7-ORF	700	PGNEPVALDM	IHMKGMAWL	NGQEIGRYWP	RRTSKYENCV	TQCDYRGKFN	749
apple	680	PGDAPLALDM	GSMKGQIWI	NGQSVGRHWP	GYIAR-GSCG	D-CSYAGTYD	729
carnation	685	GGNDPLALDL	GSMKGQAWI	NGQSIGRHWS	NNIAK-GSCN	DNCNYAGTYT	734
asparagus	681	PGNEPLALDM	NTMGKGQIWI	NGQSIGRYWP	AYKAS-GSCG	S-CDYRGTYN	730
broccoli	681	LGKDPVIDL	NGLGKGEVWI	NGQSIGRYWP	SFNSSDEGCT	EECDYRGEYG	730
Lupin	689	AGNDPLALDL	GSMKGGEVWV	NGQSIGRHWP	GNKAR-GNCG	N-CNYAGTYT	738

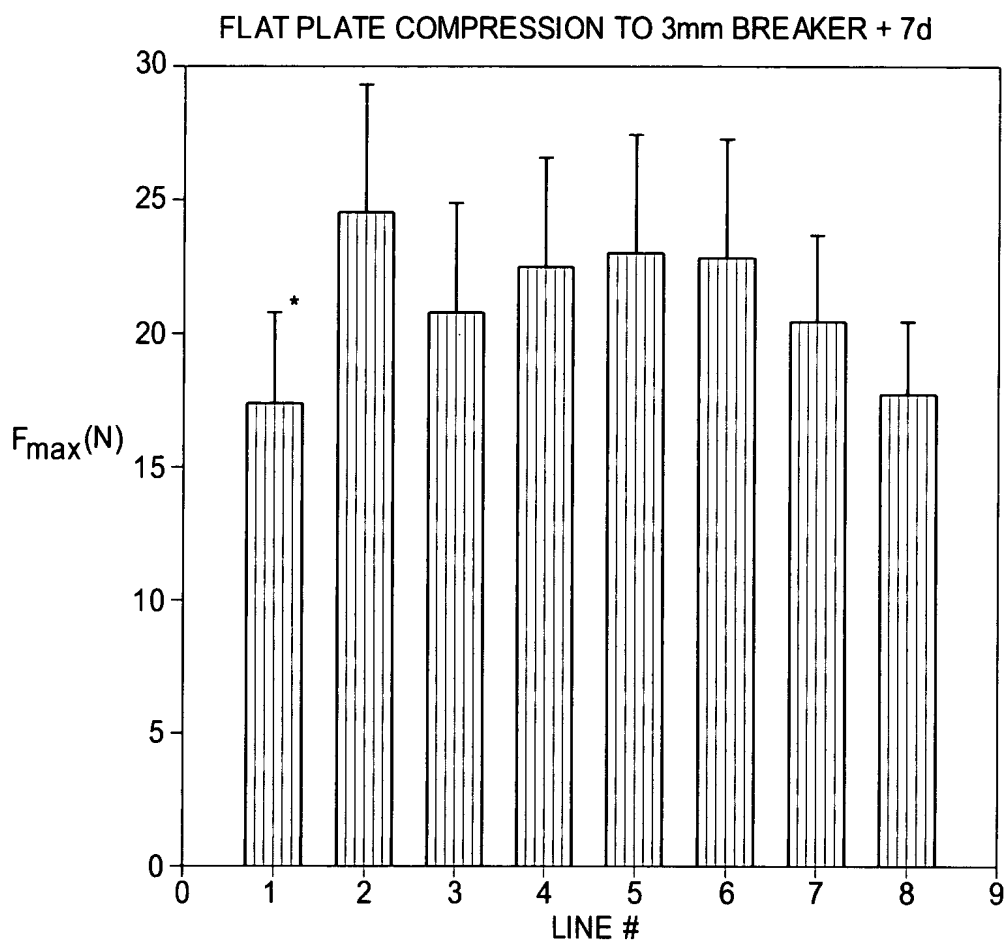
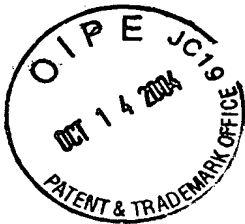
FIG. 3E

		760	770	780	790	800	
TBG1-ORF	727	EKKCLTNCGE	GSQRWYHVPR	SWLYPTGNLL	V-VFEEWGGD	PYGITLVKRE	776
TBG2-ORF	737	SDKCRTNCGE	ITQAWYHIPR	SWLKTNNVL	V-IFEETDKT	PFDISISTR	786
TBG3-ORF	731	EKKCLSNCGE	ASQRWYHVPR	SWLYPTGNLL	V-LFEEWGGE	PHGISLVKRE	780
TBG4-ORF	729	EKKCQTNCGQ	PSQRWYHVPR	SWLKPSGNLL	V-VFEEWGGN	PTGISLVRRS	778
TBG5-ORF	751	-----	-----	-----	-----	-----	800
TBG6-ORF	751	-----	-----	-----	-----	-----	800
TBG7-ORF	750	PDKCVTGCGQ	PTQRWYHVPR	SWFKPSGNVL	I-IFEEIGGD	PSQIRFSMRK	799
apple	730	DKKCRTHCGE	PSQRWYHIPR	SWLTPTGNLL	V-VFEEWGGD	PSRISLVERG	779
carnation	735	ETKCLSDCGK	SSQKWYHVPR	SWLQPRGNLL	V-VFEEWGGD	TKWVSLVKRT	784
asparagus	731	EKKCLSNCGE	ASQRWYHVPR	SWLIPTGNFL	V-VLEEWGGD	PTGISMVKRS	780
broccoli	731	SDKCAFMCGK	PTQRWYHVPR	SFLNDKGHNT	ITLFEEMGGD	PSMVKFKTVV	780
Lupin	739	DTKCLANCGQ	PSQRWYHVPR	SWLRSGGNYL	V-VLEEWGGD	PNGIALVERT	788
		810	820	830	840	850	
TBG1-ORF	777	IGSVCADIYE	WQ-PQLLNWQ	RLVSGKFDRP	LR--PKAHLK	CAPGQKISSI	826
TBG2-ORF	787	TETICAQVSE	KHYPPHLKWS	HSEFDRKLSL	MDKTPEMHLQ	CDEGHTISSI	836
TBG3-ORF	781	VASVCADINE	WQ-PQLVNWQ	MQASGKVDKP	LR--PKAHL	CASGQKITSI	830
TBG4-ORF	779	-----	-----	-----R-	-----	-----	828
TBG5-ORF	801	-----	-----	-----	-----	-----	850
TBG6-ORF	801	-----	-----	-----	-----	-----	850
TBG7-ORF	800	VSGACGHL	SV-DHPSFD--V	ENLQGSEIEN	DKNRPTLSLK	CPTNTNISSV	849
apple	780	-----	-----	-----TA	LD--AK----	-----	829
carnation	785	IA-----	-----	-----	-----	-----	834
asparagus	781	VASVCAEVEE	LQ-PTMDNWR	TKAYG-----	-R--PKVHLS	CDPGQKMSKI	830
broccoli	781	TGRVCAKAHE	-----	-----	----HNKVELS	CN-NRPISAV	830
Lupin	789	-----	-----	-----	-----	-----	838
		860	870	880	890	900	
TBG1-ORF	827	KFASFGTPEG	VCGNFQQGSC	HAPRSYDAFK	K-----NCVG	KESCSVQVTP	876
TBG2-ORF	837	EFASYGSPNG	SCQKFSQGKC	HAANSLSV--	---VSQACIG	RTSCSIGISN	886
TBG3-ORF	831	KFASFGTPQG	VCGSFREGSC	HAFHSYDAFE	R-----YCIG	QNSCSVPVTP	880
TBG4-ORF	829	-----	-----	-----	-----	-----	878
TBG5-ORF	851	-----	-----	-----	-----	-----	900
TBG6-ORF	851	-----	-----	-----	-----	-----	900
TBG7-ORF	850	KFASFGNPNG	TCGSYMLGDC	HDQNSAALVE	K-----VCLN	QNECALEMSS	899
apple	830	-----	-----	-----	-----	-----	879
carnation	835	-----	-----	-----	-----	-----	884
asparagus	831	KFASFGTPQG	TCGSFSEGSC	HAHKS YDAFE	QEGLMQNCVG	QEFCSVNVAP	880
broccoli	831	KFASFGNPSG	QCGSFAAGSC	EGAKDAVKV-	----VAKECVG	KLNCTMNVS	880
Lupin	839	-----	-----	-----	-----	-----	888

FIG. 3F

		910	920	930	940	950	
TBG1-ORF	877	ENFGGDP-CR	NVLKKLSVEA	ICS-----	----.	926
TBG2-ORF	887	GVFG-DP-CR	HVVKSLAVQA	KCSPPDLST	SASS.	936
TBG3-ORF	881	EIFGGDP-CP	HVMKKLSVEV	ICS-----	----.	930
TBG4-ORF	879	-----	-----	-----	----.	928
TBG5-ORF	901	-----	-----	-----	----.	950
TBG6-ORF	901	-----	-----	-----	----.	950
TBG7-ORF	900	ANFNMQL-CP	STVKKLAVEV	NCS-----	----.	949
apple	880	-----	----KL----	-----	----.	929
carnation	885	-----	-----	-----	----.	934
asparagus	881	EVFGGDP-CP	GTMKKLAVEA	ICE-----	----.	930
broccoli	881	HKFGSNLDCG	DSPKRLFVEV	EC-----	----.	930

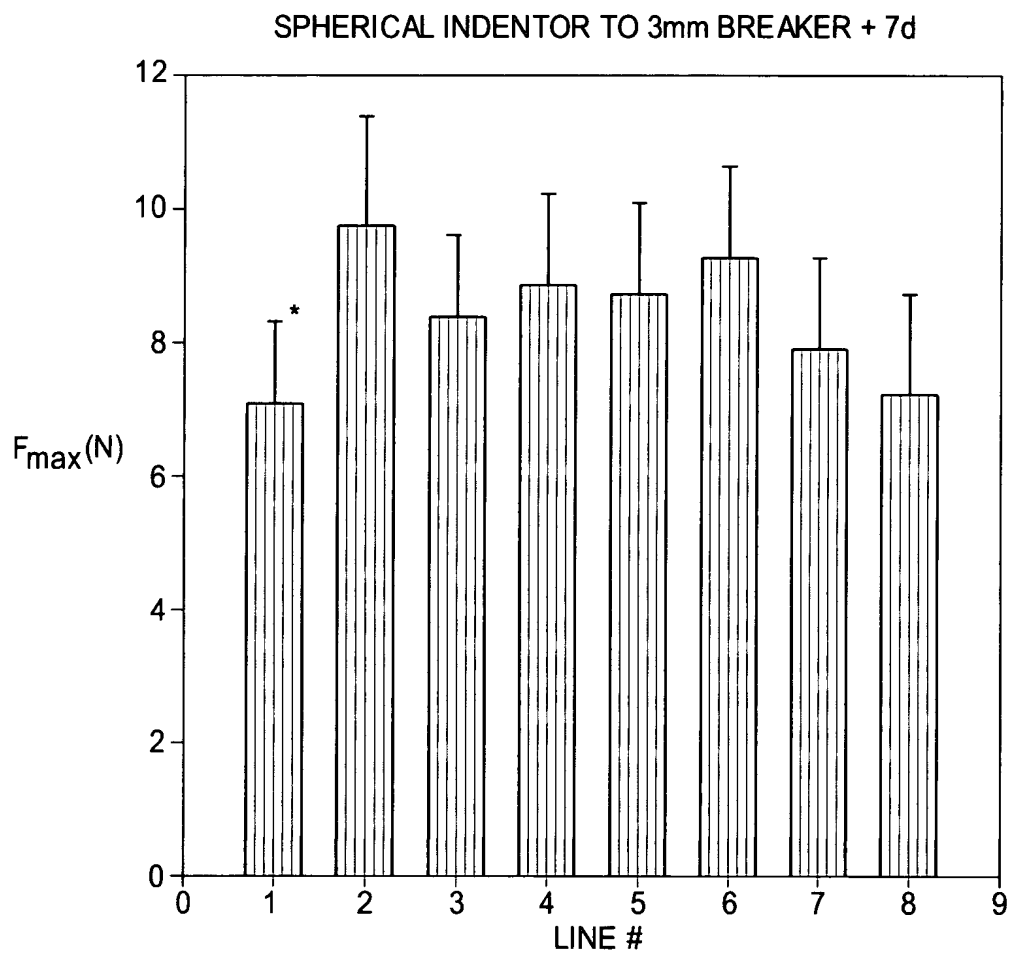
FIG. 3G



* STANDARD DEVIATION

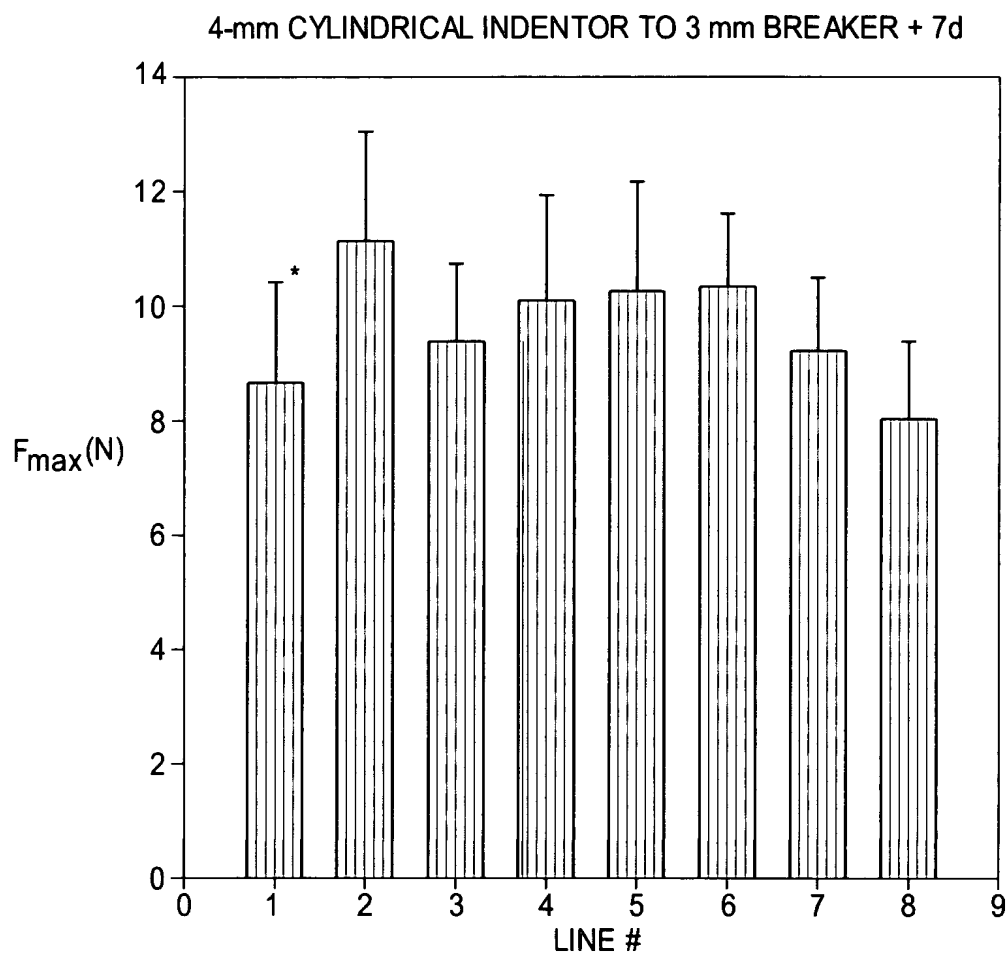
FP07 LINE#	FP07 MEAN	FP07 STD DEV
1	17.52665	3.418542
2	24.56026	4.786548
3	20.81681	4.066194
4	22.54655	4.15923
5	23.03255	4.493091
6	22.84338	4.517462
7	20.36124	3.24608
8	17.81924	2.665468

FIG. 11A



* STANDARD DEVIATION	SP07 LINE#	SP07 MEAN	SP07 STD DEV
	1	7.02	1.22
	5	9.77	1.57
	6	8.43	1.15
	7	8.87	1.32
	8	8.78	1.36
	9	9.28	1.29
	11	7.96	1.30
	12	7.26	1.45

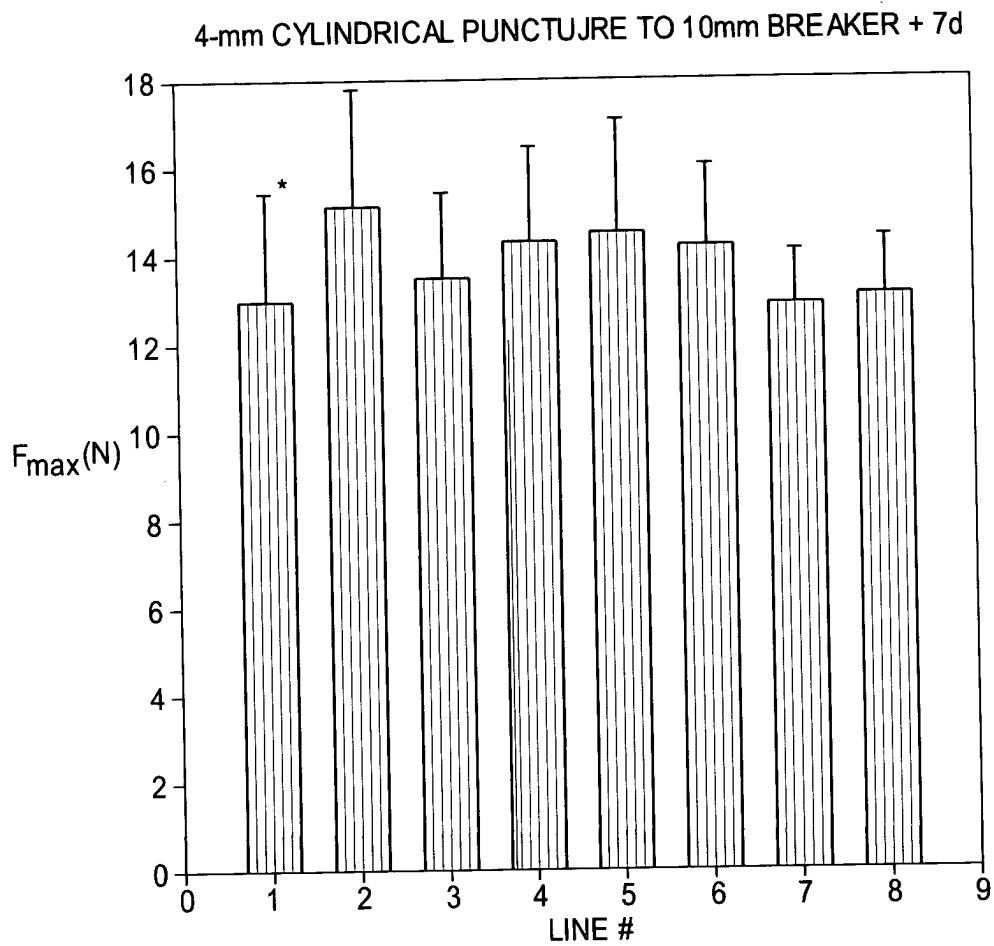
FIG. 11B



* STANDARD DEVIATION

CY07 LINE#	CY07 MEAN	CY07 STD DEV
1	8.62	1.69
5	11.07	1.96
6	9.31	1.33
7	10.07	1.81
8	10.18	1.88
9	10.27	1.26
11	9.15	1.30
12	7.99	1.33

FIG. 11C



* STANDARD DEVIATION

PU07 LINE#	PU07 MEAN	PU07 STD DEV
1	12.91	2.43
5	15.13	2.61
6	13.44	1.90
7	14.28	2.16
8	14.47	2.58
9	14.14	1.81
11	12.90	1.20
12	13.18	1.25

FIG. 11D

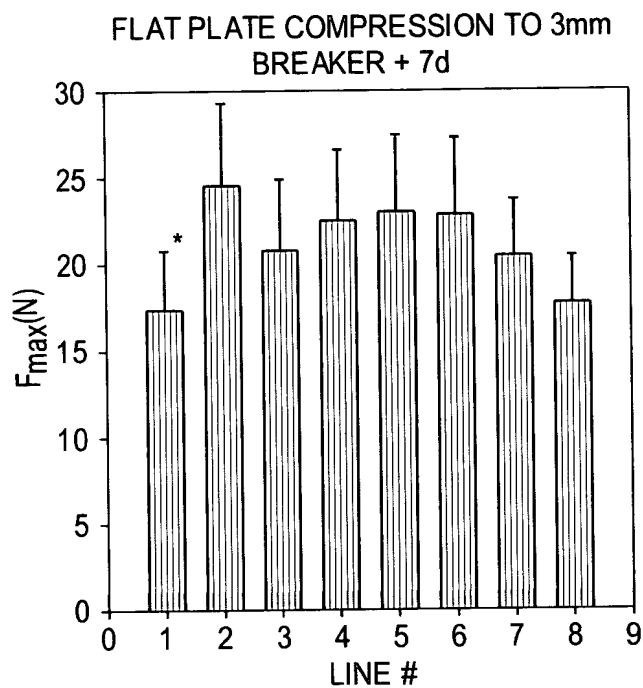


FIG. 11E(1)

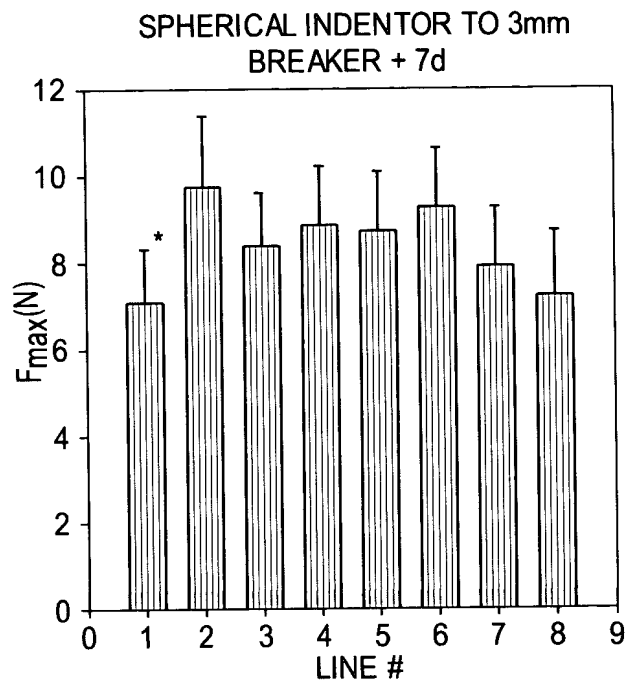


FIG. 11E(2)

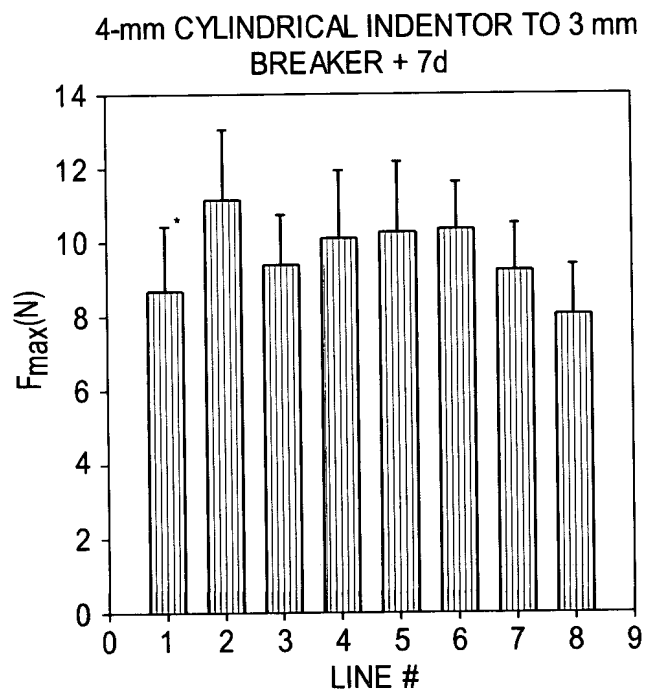


FIG. 11E(3)

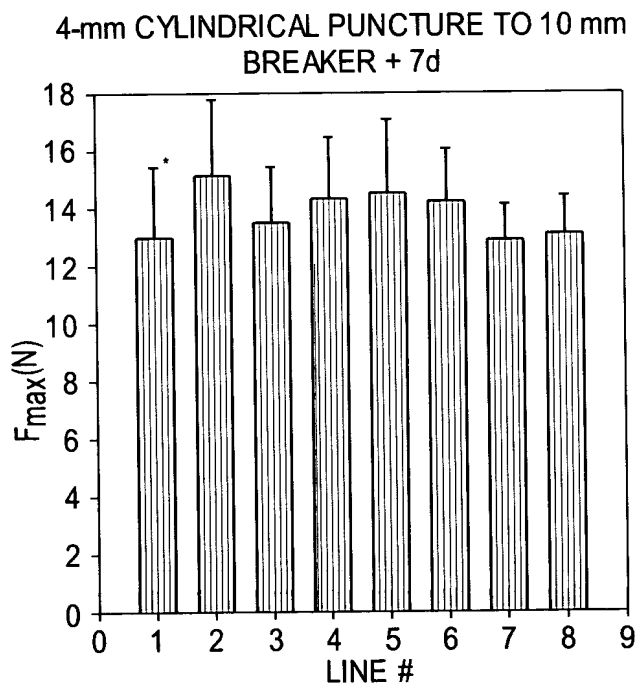


FIG. 11E(4)

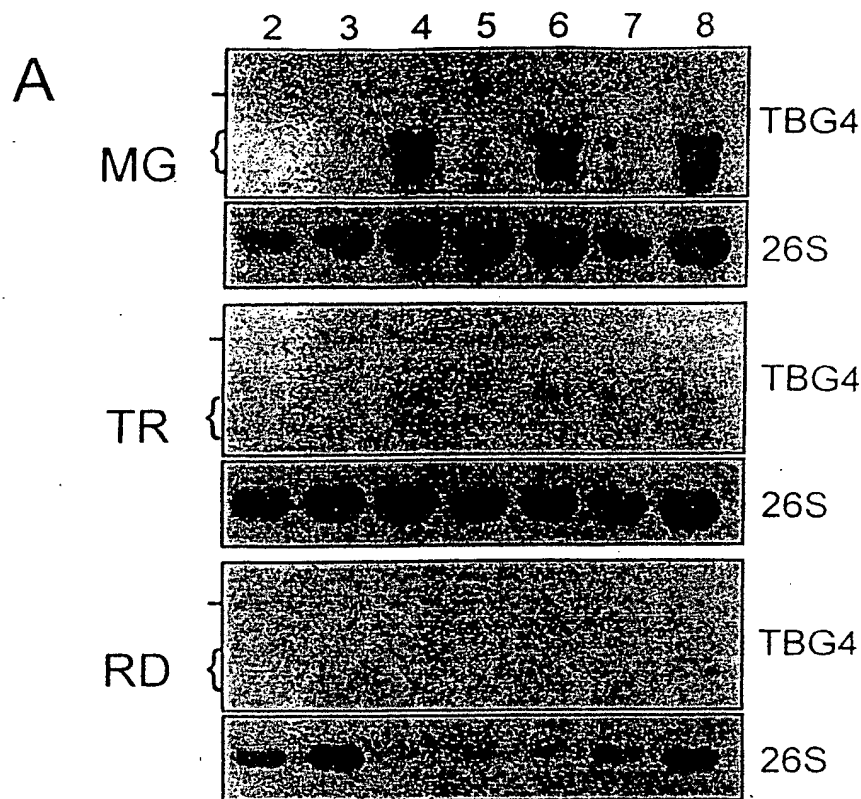


FIG. 12A

Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct. A. Total RNA was extracted from mature green/42 days post-pollination (MG), turning/breaker + 3 (TR) and red/breaker + 7 (RD) fruit and twenty μ g was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control. The marks - and { denote the positions of the endogenous TBG4 and antisense mRNAs respectively. Lanes 2-8 correspond to transgenic lines 2-8 in Figures 11A-E.

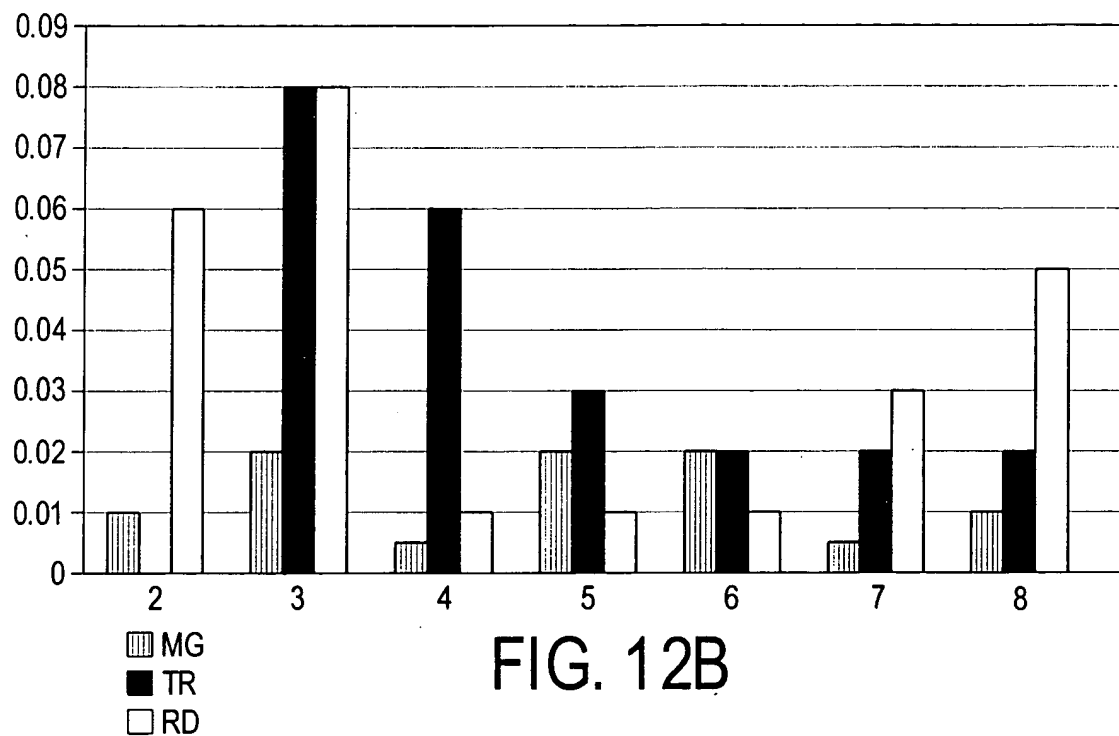


Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct.

B. Chart of TBG4

mRNA levels in lines 2-8. Autoradiographs were scanned using a densitometer and TBG4 mRNA levels were corrected against the loading controls. TBG4 mRNA levels are shown in arbitrary units.

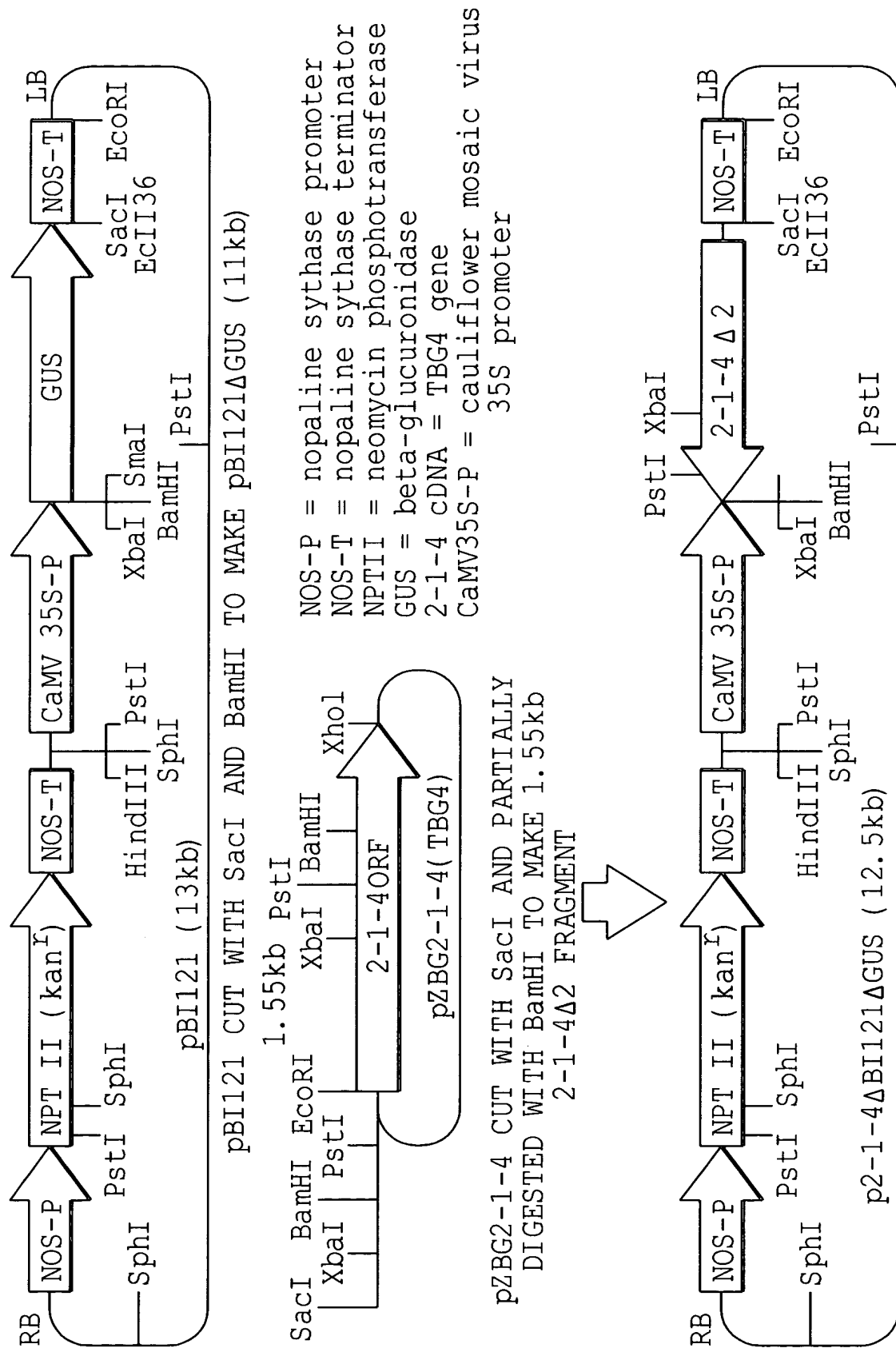
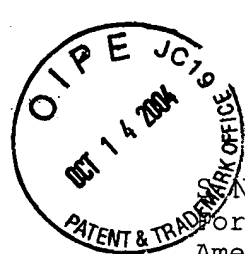


FIG. 13 BINARY CONSTRUCT USED TO TRANSFORM PLANTS AND EXPRESS TBG4
 (pZBG2-1-4 IN THE ANTISENSE ORIENTATION)



S.N. 09/701,868

Formalized Drawings (45 sheets) (Figures 1,2,3,11,12 &13)
Amendment (37 CFR 1.312(a))

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* K. Gross et al. *
* (Name of applicant, assignee, or Registered Representative) *
* *Colleen J. Gross* 10-12-04 *
* (Signature) (Date) *
